



XX WO933767-A1.  
 XX 29-JUL-1999.  
 XX  
 PF 24-JUL-1998; 98WO-JP033328.  
 XX  
 PR 23-JAN-1998; 98JP-0011281.  
 XX  
 PA (FUSO ) FUSO PHARM IND LTD.  
 XX  
 PI Wakamiya N.  
 XX  
 DR WPI: 1999-458691/38.  
 DR P-PSDB; AAY25518.  
 XX  
 PT New collectin protein of human origin and DNA encoding it  
 XX  
 PS Claim 2: Page 39-42; 58pp; Japanese.  
 CC This invention describes the isolation and characterization of a novel  
 CC human collectin protein and its encoding polynucleotide. The human  
 CC collectin exhibits antibacterial and antiviral activity and can be used  
 CC as an agent for the treatment of human bacterial and viral infections.  
 CC This sequence encodes the novel human collectin.  
 XX  
 SQ Sequence 1595 BP; 444 A; 322 C; 382 G; 447 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 6,63e-133 Length: 1595  
 Score: 1484.00 Matches: 277  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-600-932-2 (1-277) x AAX8323 (1-1595)  
 QY 1 MetAsnGlyPheAlaSerLeuLeuArgAsnGlnPheIleLeuValLeuPheLeu 20  
 DB 6 ATGAAATGGCTTGGCTTCCTTCCTCGAAGAAACCAATTATCCCTCGTGTCTTTCTT 65  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrIleAlaGlyValAla 40  
 DB 66 TTGCAAAATTCAGAGTCTGCTGTGATATGATACCGCTCTACCGCTGAAGTCTGTGCC 125  
 QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGlyGlyGlyGlyGlyGlyGly 60  
 DB 126 ACACACACAAATTTCCACGAGCCCAAGAGATGATGTTGAAAAAGAGATCCAGAGAA 185  
 QY 61 GlnGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyIleLysGlyGlyLeuGly 80  
 DB 186 GAGGGAAAGATGCGCAAGTGGAGCGATGGGCCGCAAAAGAAATTAAGGAAAGTGGGT 245  
 QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyAspLys 100  
 DB 246 GATATGGAGATCGGGGCAATATTTGGCAAGCTGGGCCCATTTGGGAAGAGGTGACAAA 305  
 QY 101 GlyGlyLysGlyLeuLeuGlyIleProGlyLysGlyLysGlyLysAlaGlyThrValCysAsp 120  
 DB 306 GGGGAAAAAGGTTTCTTGGATACCTCGAATAAAGCAAGCAAGAGTGTGTGAT 365  
 QY 121 CysGlyArgGlyArgLysPheValGlyIleLeuAspIleSerIleAlaArgLeuLysThr 140  
 DB 366 TGTGGAAGATACCGGAAATTTGTTGGACAACTGGGATATATATATGCCCCGCTCAACAA 425  
 QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyLysThrGlyLysPheThr 160  
 DB 426 TGTATGAAGTTTGTCAAAATGTGTATACAGAGATGAGGAAAGTGAAGAAATTTCTAC 485  
 QY 161 TyrIleValGlnGlyLysAsnTyrArgGlySerLeuThrHisCysArgIleArgGly 180  
 DB 486 TACATCGTCAGAGAGAGAAAGAACTACAGGAAATCCCTAACCCACCTCAGAGATTGGGGT 545

QY 181 GlyMetLeuAlaMetProLysAspGluAlaIleAsnThrLeuIleAlaAspThrValAla 200  
 DB 546 GGAATCTAGCCATGCTGCCAAGATGAGTACCTGCCACACACTATGCTGATGTGCTGC 605  
 QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
 DB 606 AAGAGTGGCTTCTTGGGTGTTCATTGGCGTGAATGACCTTGAAGAGGAGGAGACATAC 665  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTrpAsnGlnGlyLysProSer 240  
 DB 666 ATGTTCAACAGACACACTCCACTGACAGAACTATAGCACTGGAATGAGGGGACCCACAC 725  
 QY 241 AspProGlyGlyHisGluAspCysValGluMetLeuSerSerGlyArgTrpAsnAspThr 260  
 DB 726 GACCCCTATGCTATGAGAGCTGTGAGAGATGCTGAGCTGTGCGCAGATGAGATGACACA 785  
 QY 261 GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLys 277  
 DB 786 GAGTGCATCTTACCATGTACTTGTGTGATGATTCATCAAGAGAAAAAG 836  
 RESULT 2  
 AA233973  
 ID AA233973 standard; cDNA; 1016 BP.  
 AC AA233973;  
 DT 07-DEC-1999 (first entry)  
 XX  
 DE Human PRO702 nucleotide sequence.  
 XX  
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridization;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9446281-A2.  
 PD 16-SEP-1999.  
 XX  
 XX  
 PF 08-MAR-1999; 99WO-US05028.  
 XX  
 PR 10-MAR-1998; 98US-0077450.  
 PR 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077641.  
 PR 12-MAR-1998; 98US-0077791.  
 PR 13-MAR-1998; 98US-0078004.  
 PR 17-MAR-1998; 98US-0040220.  
 PR 20-MAR-1998; 98US-0078886.  
 PR 20-MAR-1998; 98US-0078910.  
 PR 20-MAR-1998; 98US-0078936.  
 PR 20-MAR-1998; 98US-0078939.  
 PR 25-MAR-1998; 98US-0079294.  
 PR 26-MAR-1998; 98US-0079656.  
 PR 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079689.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079786.  
 PR 30-MAR-1998; 98US-0079920.  
 PR 30-MAR-1998; 98US-0079923.  
 PR 31-MAR-1998; 98US-0080105.  
 PR 31-MAR-1998; 98US-0080107.  
 PR 31-MAR-1998; 98US-0080165.  
 PR 31-MAR-1998; 98US-0080194.  
 PR 01-APR-1998; 98US-0080327.  
 PR 01-APR-1998; 98US-0080328.  
 PR 01-APR-1998; 98US-0080333.  
 PR 01-APR-1998; 98US-0080334.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081049.

PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082568.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 23-APR-1998; 98US-0082766.  
 PR 27-APR-1998; 98US-0083336.  
 PR 28-APR-1998; 98US-0083332.  
 PR 29-APR-1998; 98US-0083352.  
 PR 29-APR-1998; 98US-0083495.  
 PR 29-APR-1998; 98US-0083496.  
 PR 29-APR-1998; 98US-0083499.  
 PR 29-APR-1998; 98US-0083500.  
 PR 29-APR-1998; 98US-0083545.  
 PR 29-APR-1998; 98US-0083554.  
 PR 29-APR-1998; 98US-0083558.  
 PR 29-APR-1998; 98US-0083559.  
 PR 30-APR-1998; 98US-0083742.  
 PR 05-MAY-1998; 98US-0084366.  
 PR 06-MAY-1998; 98US-0084414.  
 PR 06-MAY-1998; 98US-0084441.  
 PR 07-MAY-1998; 98US-0084598.  
 PR 07-MAY-1998; 98US-0084600.  
 PR 07-MAY-1998; 98US-0084637.  
 PR 07-MAY-1998; 98US-0084637.  
 PR 07-MAY-1998; 98US-0084639.  
 PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085323.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
 PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085589.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086022.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 22-MAY-1998; 98US-0086486.  
 PR 28-MAY-1998; 98US-0087096.  
 PR 28-MAY-1998; 98US-0087106.  
 PR 28-MAY-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Wood Wt, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 XX  
 XX WPI, 1999-551358/46.  
 XX P-PSDB; AA41698.  
 XX  
 XX New secreted and transmembrane polypeptides and their polynucleotides,  
 XX useful for treating blood coagulation disorders, cancers and cellular  
 XX adhesion disorders.  
 XX  
 XX Claim 2; Fig 36; 530P; English.  
 XX  
 XX The present invention describes secreted and transmembrane polypeptides

CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AA23391 to  
 CC AA23338, and AA41685 to AA41774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 5,39e-132 Length: 1016  
 Score: 1472.00 Matches: 275  
 Percent Similarity: 99.648 Conservative: 1  
 Best Local Similarity: 99.288 Mismatches: 0  
 Query Match: 99.194 Indels: 0  
 DB: Gaps: 0  
 US-09-600-932-2 (1-277) x AA233973 (1-1016)  
 QY 1 MetanGlyPheAlaSerLeuValArgArgAsnGlnPheIleLeuValLeuPheLeu 20  
 DB 22 ATGAATGGCTTTCATCTTGCCTTCGAAACCAATTAATCTCTGTAATCTTCT 81  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGlnValCysAla 40  
 DB 82 TTCGAATTCACAGTCGTGGCTGCTGATATTGATAGCCGCTACCCGCTGAATCTGTGCC 141  
 QY 41 ThrHisThrIleSerProGlyProGlyGlyAspAspGlyGlyGlyGlyAspProGlyGlu 60  
 DB 142 ACACACACAAATTCACACAGACCCAAAGAGATGATGGAAGAAAGAGATCCAGAGAA 201  
 QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyAlaGlyGlyGlyGlyGly 80  
 DB 202 GAGGAAACGATGCGCAATGGAGCGATGGGCGCCGAAAGAAATTAAGAGAACTGGGT 261  
 QY 81 AspMetGlyAspArgGlyLysAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100  
 DB 262 GATATGGAGATCAGGCGCAATGATGAGCAAGATGGCCCATGGGAGAGAGGTGACAAA 321  
 QY 101 GlyGlyLysGlyLeuLeuGlyLysLeuProGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
 DB 322 GGGGAAAGAGGTTTGGTGAATACCTGGAGAAAGGCAAGGCAAGGCTGTGTGTGT 381  
 QY 121 CysGlyArgTyrArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuArgThr 140  
 DB 382 TGTGGAAGATACCGGAATTTGTGGACAACGTGATATTAGTATGCTGGCTCAAGACA 441  
 QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlnThrGlnLysPheTyr 160  
 DB 442 TCTATGAAGTTTGTCAAGATGATGATGAGGAGGATTAAGGAAACGTAAAGAAATTCAC 501  
 QY 161 TyrIleValGlnGlnLysLysAsnTyrArgGlnSerLeuThrHisCysArgIleArgGly 180  
 DB 502 TACATGCTGAGGAAGAAGAAAGAACTACAGGAACTCCATACCCACGCGAGATGGGGT 561  
 QY 181 GlyMetLeuAlaMetProLysAspGlnAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
 DB 562 GGAATGCTAGCCATGGCCCAAGGATGAGCTGCCAACAACCTATGCTCTATGTGGC 621  
 QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlnArgGlnGlyGlnTyr 220  
 DB 622 AAGAGTGGCTTCTTGGGCTTCATTCGCGTGAATGACCTTGAAAGGAGGAGACAGTAC 681  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrAsnGlnGlyLupProSer 240  
 DB 682 ATGTCACACAGACACACTCCACTGCAAGAACTATAGCAACTGGAATGAGGGAGAACCCAC 741  
 QY 241 AspProTyrGlyHisGlnAspCysValGlnMetLeuSerSerGlyArgTyrAsnAspThr 260



XX AC AAS45974;  
XX DT 18-DEC-2001 (first entry)  
XX DE Human DNA encoding PRO polypeptide sequence #50.  
XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;  
KW PCR primer.  
XX OS Homo sapiens.  
XX PN WO200168848-AZ.  
XX PD 20-SEP-2001.  
XX PF 28-FEB-2001; 2001WO-US06520.  
XX PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 03-MAR-2000; 2000US-187202P.  
PR 06-MAR-2000; 2000US-186968P.  
PR 14-MAR-2000; 2000US-189320P.  
PR 14-MAR-2000; 2000US-189328P.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000US-190828P.  
PR 21-MAR-2000; 2000US-191007P.  
PR 21-MAR-2000; 2000US-191048P.  
PR 21-MAR-2000; 2000US-191314P.  
PR 28-MAR-2000; 2000US-192555P.  
PR 29-MAR-2000; 2000US-193032P.  
PR 29-MAR-2000; 2000US-193053P.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 04-APR-2000; 2000US-194449P.  
PR 04-APR-2000; 2000US-194479P.  
PR 11-APR-2000; 2000US-195975P.  
PR 11-APR-2000; 2000US-196000P.  
PR 11-APR-2000; 2000US-196187P.  
PR 11-APR-2000; 2000US-196690P.  
PR 11-APR-2000; 2000US-196820P.  
PR 18-APR-2000; 2000US-198121P.  
PR 18-APR-2000; 2000US-198585P.  
PR 25-APR-2000; 2000US-199397P.  
PR 25-APR-2000; 2000US-199550P.  
PR 25-APR-2000; 2000US-199549P.  
PR 03-MAY-2000; 2000US-201516P.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 05-JUN-2000; 2000US-202632P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 22-AUG-2000; 2000US-064484P.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
XX PA (GENE ) GENENTECH INC.  
XX PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX DR MPI: 2001-602746/68.  
XX DR P-PSDB; A029073.  
XX PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumours, such as prostate and breast tumours, in mammals and  
PT to screen for modulators of the compounds -

PS Claim 2; Fig 99; 774pp; English.  
XX CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
CC primers for PRO polypeptides of the invention. The sequences of the  
CC invention can be used to detect the presence of a tumour in a mammal by  
CC comparing the level of expression of a PRO polypeptide in a test sample  
CC of cells from the animal and a control sample of normal cells, whereby a  
CC higher level of expression in the test sample indicates the presence of a  
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
CC blood, when contacted with it. A specific polypeptide can be used to  
CC stimulate the proliferation or differentiation of chondrocyte cells. The  
CC PRO proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders.  
XX SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 5 39e-132 Length: 1016  
XX Score: 1472.00 Matches: 275  
XX Percent Similarity: 99.64% Conservative: 1  
XX Best Local Similarity: 99.28% Mismatches: 1  
XX Query Match: 99.19% Indels: 0  
XX DB: 22 Gaps: 0  
XX  
XX US-09-600-932-2 (1-277) x AAS45974 (1-1016)  
XX  
XX QY 1 Metcansglyphealaserleuleuargarganglphelleuleuvalleupheleu 20  
XX DB 22 ATGAAATGGCTTTCACCTTCCTTCACAGAAACAAATTTATCTCTGAGTACTTCTT 81  
XX QY 21 LeuGlnIleGlnserleuGlyleuAspIleAspSerArgProthrIleGluValCysala 40  
XX DB 82 TTGCATTTTCAGACTCGGCTCGATATTGATAGCCGCTCTCCCTGAAAGCTGTGCC 141  
XX QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGluGlyGlyAspProGlyGlu 60  
XX DB 142 ACACACACAAATTTTCACAGAGCCCAAGAGAGATGATGAGAAAGAGATCCAGAGAA 201  
XX QY 61 GluGlyLysHisIleGlyLysValIleArgMetGlyProGlyGlyLysGlyGlyLeuGly 80  
XX DB 202 GAGGGAAGACATGACCAAGTGGACGATGGGCGCAAGAAATTAAGAGAACTGGGT 261  
XX QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysIleGlyAspLys 100  
XX DB 262 GATATGGAGATCAGGCAATATTGGCAAGACTGGGCCCATTTGGAAAGGATGACAAA 321  
XX QY 101 GlyGlnLysGlyLeuLeuGlyLleProGlyGlnLysGlyLysAlaGlyThrValCysasp 120  
XX DB 322 GGGGAAAAGAGTTTGGTGAATACCTGGGAAAAGGCAAAACAGAGTCTGTGTGAT 381  
XX QY 121 CysGlyArgTyrArgLysPheValIleGlnLeuAspIleSerIleAlaArgLeuLysThr 140  
XX DB 382 TGTGGAAAGATACCGGAATTTGTTGGCAACTGATATTATGTTGCTGGCTCAAGACA 441  
XX QY 141 SerMetLysPheValLysAsnValIleAlaGlyLleArgGlnThrGlnLysPheTyr 160  
XX DB 442 TCTATGAAGTTTGTCAAGATGTGATAGCGGATTAAGGAACTAAGAGAAATCTCTAC 501  
XX QY 161 TyrIleValIleGlnLysLysAsnTyrArgLysSerLeuThrHisCysArgIleArgGly 180  
XX DB 502 TACATCGTGAAGAGAGAGAACTACAGGATCCCTAACCCACGCGAGATTCGGGG 561  
XX QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
XX DB 562 GGAATGTACCACTGCGCAAGATGAAGCTGCCAACAACATCTCCTGCTGTGTGCC 621  
XX QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuLysGlnGlyGlnTyr 220

DB 622 AAGAGTGGCTTCTTCCGGGTGTCATTCGGCTGAATGACCTTGAAGGAGGACAGATAC 681  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTrpAsnGluGlnProSer 240  
 DB 662 ATGTCCACAGACACACCTCCAGACTATAGCACTGAAATGAGGGGAAACCCAGC 741  
 QY 241 AspProTyrGlyHisGluAspCysValGlnMetLeuSerSerGlyArgTrpAsnAspThr 260  
 DB 742 GACCCCTATNGGTGATGAGAGCTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801  
 QY 261 GlnCysHisLeuThrMetTyrPheValCysGluPheIleIleLysLysLys 277  
 DB 802 GAGTCCACTTACCATGTACTGTCTGTGAGTTCATCAGAGAGAAAAAG 852

## RESULT 5

ABAB1207  
 ID ABAB1207 standard; DNA; 813 BP.

XX ABA91207;

DT 19-FEB-2002 (first entry)

DE Human collectin polynucleotide SEQ ID NO 58.

KW Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;

XX protein therapy; infection; ds.

OS Homo sapiens.

PN WO200181401-A1.

PD 01-NOV-2001.

PE 23-APR-2001; 2001WO-JP03468.

PR 21-APR-2000; 2000JP-0120358.

PA (FUSO ) FUSO PHARM IND LTD.

PI Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y;

DR WPI; 2002-055345/07.

PT New collectin family proteins, designated CL-L2-1 and CL-L2-2,  
 PT expressed in kidney and for treatment and prevention of bacterial and  
 PT viral infections

PS Claim 20; Page 126-127; 134pp; Japanese.

XX The invention relates to human collectin family proteins (CL-L2-1 and  
 CC CL-L2-2, sequences given in the specification, AB556407-AB556411 and  
 CC AB556414-AB556416), their derivatives and fragments and a related  
 CC collectin (CL-L2) of mouse origin (AB556412) and polynucleotides encoding  
 CC all or part of the proteins. The proteins have antibacterial and virucide  
 CC activity and are used for protein therapy and treatment, prevention and  
 CC diagnosis of bacterial and viral infections. The present sequence is that  
 CC of a collectin polynucleotide of the invention.

SQ Sequence 813 BP; 211 A; 198 C; 252 G; 152 T; 0 other;

## Alignment Scores:

Pred. No.: 1e-60 Length: 813  
 Score: 728.00 Matches: 128  
 Percent Similarity: 72.11% Conservative: 63  
 Best Local Similarity: 51.00% Mismatches: 64  
 Query Match: 49.06% Indels: 7  
 DB: 24 Gaps: 2

US-09-600-932-2 (1-277) x ABA91207 (1-813)

QY 28 LeuAspIleAspSerArgProThrAlaGluValCysAlaThrHisThrIleSerProGly 47  
 DB 65 CTGATGTCCTCAGACAGACACA-GAGGAGCGCTGCTCTGTGAGATTCCTGCCCCGGC 123

QY 48 ProLysGlyAspAspGlyGluLysGlyAspProGlyGluGluGlyHisGlyVal 67  
 DB 124 CTCAAAAGGGATCAGAGAAAAGGAGAC-----AAAGGAGCCCCAGAGGCCA 174  
 QY 68 GlyArgMetGlyProLysGlyIleLysGlyGluLeuGlyAspMetGlyAspArgGlyAsn 87  
 DB 175 GGAAGAGTGGCCCTACAGAGAAAAGGAGACATGGGGGACAAAAGACAGAAAGGCACT 234  
 QY 88 Ile-----GlySerThrGlyProIleGlyLysLysGlyAspLysGlyGluGly 104  
 DB 235 GTGGGCCGCCCATGGAATAATGGTCCCATGGCGCAAAAGGGAATAAGACATCTGTGT 294  
 QY 105 IleuLeuGlyIleProGlyGluLysGlyLysAlaGlyThrValCysAspCysGlyArgTyr 124  
 DB 295 GATATCGGACCCCTGGCCCCAGTAGAGAAACCTGATATTCATGTGATGAGTCAGTCAGCG 354  
 QY 125 ArgLysPheValGlyGluLeuAspIleSerIleAlaArgLeuLysThrSerMetLysPhe 144  
 DB 355 AGGAGGCTATTTGGGAGATGACCAACAGGTCCTCACTCACTGACAACTGAGCTAAATTC 414  
 QY 145 ValLysAsnValIleAlaGlyIleArgGlyLeuThrGluGluLysPheTyrTrpIleValGln 164  
 DB 415 ATAAAAAATGCTGTCTGCTGCGCGCCGAGACTGAGACAGCAAGATCTACCTGCTGTGAAG 474  
 QY 165 GlnGluLysAsnTyrArgLysSerLeuThrHisCysArgIleArgGlyMetLeuAla 184  
 DB 475 GAGAGAGAGCGGTACCCAGATGCCAGCTGTCTGCCAAGCCCGAGCGGCACACTGAGC 534  
 QY 185 MetProLysAspGluAlaAsnThrLeuIleAlaAspTyrValAlaLysSerGlyPhe 204  
 DB 535 ATGCCCAAGACAGAGCAGCCCAATGCCCTGATGCTTCACTACCTGACAGAGGCTGGCCG 594  
 QY 205 PheArgValPheIleGlyValAsnAspLeuArgGluGlyGlnTyrMetPheThrAsp 224  
 DB 595 GCCCGAGCTTTCATCGTATCATGACCTGAGAAAGAGGTCCTTCTGTAACCTGGAGC 654  
 QY 225 AsnThrProLeuGlnAsnTyrSerAsnTrpAsnGluGluProSerAspProTyrGly 244  
 DB 655 CGCTCCCGCATGAGACCTTCAACAGATGGCGCAGTGGAGAGCCCAACAGCGCTTGAT 714  
 QY 245 HisGluAspCysValGluMetLeuSerSerGlyArgTrpAsnAspThrGluHisLeu 264  
 DB 715 GAGAGAGAGCTGTGAGATGGTGGCTGAGGCTGAGGTGAGATGATGTGCGCCGACACT 774  
 QY 265 ThrMetTyrPheValCysGluPheIleLysLys 275  
 DB 775 ACCATGACTTCAATGTGCGAGTTGACAAAGAG 807

## RESULT 6

ABAB1176  
 ID ABA91176 standard; cDNA; 1522 BP.

XX ABA91176;

DT 19-FEB-2002 (first entry)

DE Mouse collectin encoding polynucleotide SEQ ID NO 12.

KW Human; collectin; CL-L2-1; CL-L2-2; mouse; antibacterial; virucide;

XX protein therapy; infection; ss.

OS Mus musculus.

PN WO200181401-A1.

PD 01-NOV-2001.

PE 23-APR-2001; 2001WO-JP03468.

PR 21-APR-2000; 2000JP-0120358.

PA (FUSO ) FUSO PHARM IND LTD.

XX Wakamiya N, Keshi H, Ohtani K, Sakamoto T, Kishi Y;  
PI  
XX  
DR WPI: 2002-055345/07.  
P-PSDB: ABB56412.

XX New collectin family proteins, designated CL-L2-1 and CL-L2-2,  
PI expressed in kidney and for treatment and prevention of bacterial and  
XX viral infections  
XX  
PS Claim 20; Page 102-103; 134pp; Japanese.

XX The invention relates to human collectin family proteins (CL-L2-1 and  
CC CL-L2-2, sequences given in the specification, ABB56407-ABB56411 and  
CC ABB56414-ABB56416), their derivatives and fragments and a related  
CC collectin (CL-L2) of mouse origin (ABB56412) and polynucleotides encoding  
CC all or part of the proteins. The proteins have antibacterial and virucide  
CC activity and are used for protein therapy and treatment, prevention and  
CC diagnosis of bacterial and viral infections. The present sequence is that  
CC of a collectin polynucleotide of the invention.

XX Sequence 1522 BP; 425 A; 363 C; 416 G; 318 T; 0 other;

Alignment Scores:  
Pred. No.: 2.17e-60 Length: 1522  
Score: 728.00 Matches: 128  
Percent Similarity: 72.11% Conservative: 53  
Best Local Similarity: 51.00% Mismatches: 64  
Query Match: 49.06% Indels: 7  
DB: 24 Gaps: 2

US-09-600-932-2 (1-277) x ABA91176 (1-1522)

QY 28 LeuApIleAspSerArgProThrAlaGluValCysAlaThrHisThrIleSerProGly 47  
DB 221 CTGGATGCTCTCAGCAGACACACA-GAGGAGCGCTCTGCGCAGATTCTGTCGCCGCG 279  
QY 48 ProlySGlyAspAspGlyGluGlyAspProGlyGluGlyGlySHSGlyVal 67  
DB 280 CTCAGAGGGATGCGAGGAGAAAGGAGAC-----AAAGAGGCCCAAGGAGGCCCA 330  
QY 68 GlyArgMetGlyProlySGlyIleLeuGlyGluLeuGlyAspMetGlyAspArgGlyAsn 87  
DB 331 GGAAGAGTCGGCCCTACAGAGAAAGAGACATGGGGGCAAGAAAGAGCAAGAAAGCACT 390  
QY 88 Ile-----GlyIleThrGlyProIleGlyIleGlyIleGlyIleGlyIleGlyIle 104  
DB 391 GTGGGCCCGCATGGAAATTTGGTCCATTGGCGCAAAAGGTGAAAGAGGATTCGTGT 450  
QY 105 LeuLeuGlyIleProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 124  
DB 451 GATATCGGAGCCCGTGGCCCGAGGAGAACCTGTGTTCCATGTGATGAGTGCAGTCACTG 510  
QY 125 ArgIlePheValIleGlyIleLeuAspIleSerIleAlaArgLeuIleThrSerMetIlePhe 144  
DB 511 AGGAAGGCTATTGGGAGATGACACACAGGTCACTCACTCACTCACTCACTCACTCACTCA 570  
QY 145 ValIleAsnValIleAlaGlyIleArgGlyIleGlyGlyGlyGlyGlyGlyGlyGlyGly 164  
DB 571 ATAAATAATGCTGTTGCTGGCGGTGGCGAGACTGAGAGCAAGATCTACGCTGCTGAG 630  
QY 165 GluGluIleAsnIleArgIleSerLeuThrHisCysArgIleArgGlyGlyMetLeuAla 184  
DB 631 GAGGAGAAAGCGGTGCGAGTCCGCTGCGCAAGGCCCAAGGCGGAGCACTGAGC 690  
QY 185 MetProlyAspGlyAlaAlaAsnThrLeuIleAlaAspIleValAlaIleValSerGlyPhe 204  
DB 691 ATGCCCAAGAGAGAGCGAGCAATGGCTGTATGCTTCATCTCTGCGAGAGCTGGCCTG 750  
QY 205 PheArgValPheIleGlyValAlaAspIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 224  
DB 751 GCCCGAGTCTTCATCGGTATCATGACCTGAGAGAAAGAGTGTCTTCGTACTCGGAG 810

QY 225 AsnThrProLeuGlnAsnIleSerAsnIlePaspGluGluProSerAspProIleGly 244  
DB 811 CGCTCCCGCATGAGACCTTCAAGCAAGTGGCGAGTGGCCCAACACAGCTATGAT 870  
QY 245 HisGluAspCysValGluMetLeuSerSerGlyArgIlePaspAspThrGluCysHisLeu 264  
DB 871 GAGGAGAGAGCTGTGAGATGATGCGCTCAGGTCGCTGGAATGATGTGCGCCGACACT 930  
QY 265 ThrMetIlePheValCysGluPheIleIleIleIleIleIleIleIleIleIleIle 275  
DB 931 ACCATGTACTCATGTGCGAGTTTGACAAAGAG 963

# RESULT 7

AAC58385  
ID AAC58385 standard; cDNA; 1238 BP.

AC AAC58385;  
XX  
XX 29-JAN-2001 (first entry)

DE Human PRO1182 nucleotide sequence SEQ ID NO:50.

XX Human: tumour; diagnosis; neoplastic disease; neoplastic cell growth;  
KW proliferation; tumorigenesis; identification; cancer; cytostatic;  
KW neoplastic; neuroprotective; antiinflammatory; immunosuppressive;  
KW immunostimulant; antiangiogenic; leukemia; lymphoid malignancy;  
KW neuronal disorder; glial disorder; astrocytic disorder; angiogenic;  
KW hypothalamic disorder; glandular disorder; macropagal disorder;  
KW epithelial disorder; stromal disorder; blastocellic disorder;  
KW inflammatory disorder; immunologic disorder; ss.

OS Homo sapiens.  
XX  
XX NC0200053755-A2.

PN 14-SEP-2000.

PD 06-JAN-2000; 2000MO-US00376.

PE 08-MAR-1999; 99MO-US05028.

PR 02-JUN-1999; 99MO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 26-JUL-1999; 99US-0145698.

PR 30-NOV-1999; 99MO-US28313.

PR 20-DEC-1999; 99MO-US30811.

PR 05-JAN-2000; 2000MO-US00219.

XX (GENTH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;  
PI Metanabe CK, Wood WJ;

DR WPI: 2000-572270/53.

DR P-PSDB: AAB24075.

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the  
PT treatment, diagnosis and prevention of cancer -

PS Claim 50; Fig 37; 286pp; English.

XX The present invention describes an isolated antibody that binds to  
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO353,  
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,  
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,  
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,  
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell  
CC growth. The PRO polypeptides and nucleotides are useful in the  
CC treatment, diagnosis and prevention of cancer. The antibodies and other  
CC anti-tumour compounds may be used to treat various conditions, including  
CC those characterised by overexpression and/or activation of the amplified  
CC PRO genes. Exemplary conditions or disorders to be treated with such  
CC antibodies and other compounds include benign or malignant tumours





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PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 25-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090696.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 07-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 09-JUL-1998; 98US-0091982.
PR 10-JUL-1998; 98US-0092182.
PR 20-JUL-1998; 98US-0093472.
PR 20-JUL-1998; 98US-0093439.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.

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PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 98US-0113565.
PA (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WL, Yuan J;
XX WPI: 2000-072883/06.
DR P-PSDB; AAY66738.
PT
XX Membrane-bound proteins and related nucleotide sequences
XX Claim 2; Fig 251; 822pp; English.
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 1238 BP; 293 A; 321 C; 389 G; 235 T; 0 other;
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Score: 719.50 Matches: 130
Percent Similarity: 67.74% Conservative: 59
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DB 46 GGTCTCTGCTGCGCTGAGATGAGGGGATGAGCCCTGGGCTTCATATAGC 105
QY 23 IleGlnSerLeuGlyLeuAspLleAspSerArGProThrAla-----GluValCys 39
DB 106 CTGGCCTTCCTGTCACGCTGCATCTGCACATCTCAGCCGCTGCGATGACGCTGC 165
QY 40 AlaThrHsrHrLieserProGlyProLysGlyAspAspLysGlyAspProGly 59
DB 166 TCTGTGAGATCTCTGCTCCCTGCTCAAGGGGATCGGAGAGAGAGAC----- 219
QY 60 GluGluGlyLysHsLsGlyLysValGlyArgMetGlyProLysGlyLysGlyLys 79
DB 220 ---AAAGGCGCCCGGAGCGGCTGGAAGTGTGCGCCCAAGGAGGAGAGAGACATG 276

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GenCore version 5.1.6  
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14: /cgn2.6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	1472	99.2	1016	9	US-09-999-832A-96

5	1472	99.2	1016	9	US-09-978-189-96	Sequence 96, Appl
6	1472	99.2	1016	9	US-10-174-590-99	Sequence 99, Appl
7	1472	99.2	1016	9	US-10-176-738-99	Sequence 99, Appl
8	1472	99.2	1016	9	US-10-175-737-99	Sequence 99, Appl
9	1472	99.2	1016	9	US-10-173-706-99	Sequence 99, Appl
10	1472	99.2	1016	9	US-10-175-738-99	Sequence 99, Appl
11	1472	99.2	1016	9	US-10-175-752-99	Sequence 99, Appl
12	1472	99.2	1016	9	US-10-176-482-99	Sequence 99, Appl
13	1472	99.2	1016	9	US-10-176-757-99	Sequence 99, Appl
14	1472	99.2	1016	9	US-10-176-913-99	Sequence 99, Appl
15	1472	99.2	1016	9	US-10-180-552-99	Sequence 99, Appl
16	1472	99.2	1016	9	US-10-180-557-99	Sequence 99, Appl
17	1472	99.2	1016	9	US-10-173-700-99	Sequence 99, Appl
18	1472	99.2	1016	9	US-10-174-572-99	Sequence 99, Appl
19	1472	99.2	1016	9	US-10-174-579-99	Sequence 99, Appl
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21	1472	99.2	1016	9	US-10-174-588-99	Sequence 99, Appl
22	1472	99.2	1016	9	US-10-175-739-99	Sequence 99, Appl
23	1472	99.2	1016	9	US-10-175-740-99	Sequence 99, Appl
24	1472	99.2	1016	9	US-10-175-743-99	Sequence 99, Appl
25	1472	99.2	1016	9	US-10-176-488-99	Sequence 99, Appl
26	1472	99.2	1016	9	US-10-176-492-99	Sequence 99, Appl
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31	1472	99.2	1016	9	US-10-176-991-99	Sequence 99, Appl
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33	1472	99.2	1016	9	US-10-176-993-99	Sequence 99, Appl
34	1472	99.2	1016	9	US-10-184-658-99	Sequence 99, Appl
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39	1472	99.2	1016	9	US-10-174-585-99	Sequence 99, Appl
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42	1472	99.2	1016	9	US-10-175-748-99	Sequence 99, Appl
43	1472	99.2	1016	9	US-10-176-485-99	Sequence 99, Appl
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45	1472	99.2	1016	9	US-10-176-493-99	Sequence 99, Appl

## ALIGNMENTS

RESULT 1  
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: Patent No. US20020156006A1  
: GENERAL INFORMATION:  
: APPLICANT: Ashkenazi, Avi  
: APPLICANT: Baker, Kevin P.  
: APPLICANT: Bostein, David  
: APPLICANT: Desnoyers, Luc  
: APPLICANT: Eaton, Dan  
: APPLICANT: Ferrara, Napoleon  
: APPLICANT: Filvaroff, Ellen  
: APPLICANT: Fong, Sherman  
: APPLICANT: Geo, Wei-Oiang  
: APPLICANT: Gerber, Hanspeter  
: APPLICANT: Gettsen, Mary E.  
: APPLICANT: Goddard, Audrey  
: APPLICANT: Godowski, Paul J.  
: APPLICANT: Grimaldi, J. Christopher  
: APPLICANT: Gurney, Austin L.  
: APPLICANT: Hillan, Kenneth J.  
: APPLICANT: Kijavini, Ivar J.  
: APPLICANT: Kuo, Sophia S.  
: APPLICANT: Napier, Mary A.  
: APPLICANT: Pan, James  
: APPLICANT: Paonli, Nicholas F.  
: APPLICANT: Roy, Margaret Ann  
: APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630P1C11  
 CURRENT APPLICATION NUMBER: US/09/978,295A  
 PRIOR FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
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 PRIOR FILING DATE: 1998-03-12  
 PRIOR APPLICATION NUMBER: 60/078004  
 PRIOR FILING DATE: 1998-03-13  
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 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078936  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078939  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079656  
 PRIOR FILING DATE: 1998-03-26  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2,666-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.64% Conservative: 1  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 99.19% Indels: 0  
Gaps: 0

US-09-600-932-2 (1-277) x US-09-978-295A-96 (1-1016)

QY 1 Metannglyphealaserleuleuargyasnlnpheileleuleuvalleupheleu 20  
DB 22 ATGAATGGCTTGCATCCTTCCTCGAAGAAACCAATTATCCCTCGGACATATCTT 81  
QY 21 Leuglnleuglnserleuglyleuasplleaspearrprohrralaglualcyala 40  
DB 82 TTGCAATTCAGAGCTGGCTGCTGATATTGATAGCCGCTCTACCGTGAAGTGTGCC 141  
QY 41 Thrhsthrllieserproglyprolysglyaspspelyglulysglyaspptrogllyglu 60  
DB 142 ACACACACAAATTTACACCGACCCCAAGAGAGATGTGTAAAAAGAGATCCAGGAGAA 201  
QY 61 Gluglylyshlsaglylyvalygllyargmetglyprolysglylylelysglygluleugly 80  
DB 202 GAGGAGAAAGCATGGCAAGTGCGACCATGGGCCGGAAGAAATTAAAGGAGAACTGGCT 261  
QY 81 Aspmetglyasparaglyasnlnlelylysthrlyprolelygllylysglyasplys 100  
DB 262 GATATGGAGATCAGGCGCAATATGGCAAGACTGGCCCATTTGGAAGAGAGGAGAAA 321  
QY 101 Glylylyshlsaglylyleuleuglyleproglylylysglylyasgllythvalcyasp 120  
DB 322 GGGGAAAAAGGTTGCTTGGAATACCTGGAGAAAAAGCAAGAGGAGGAGTGTGTGAT 381  
QY 121 Cysglyarglyarglyphevalygllylnleuasplleserlealearglyleuylthr 140  
DB 382 TGTGAAAGATACCGGAAATTTGTTGGACAACTGATATTAGTGTGCTCGGCTCAAGACA 441  
QY 141 Sermetlysphevalylyasnlnvalilleaglylearglyluthrglyluphphyr 160  
DB 442 TCTAAGAAAGTTGTCAAAATGTGTAGCAGGAGATAGGAGAACTGAAAGAAATTTCTAC 501  
QY 161 Tyrillevalglnglyllyasnlnlyarglyluserleuthrthscysargyleargly 180

DB 502 TACATGCTGACAGAGAGAAAGAACTACAGGAGATCCCTAACCCACTGACGAGATTCGGGGT 561  
QY 181 GlyMetleuAlametrolyaspglyuaialaasnThleuileAlaasplyrVala 200  
DB 562 GGAATGCTAGCATTGCGCAAGAGTGAAGTGCACACACTCATGCTGATCTGTGCGC 621  
QY 201 lysSerglyphehrrgvalpheiileglyvalasnaspleugluargsluglylnlyr 220  
DB 622 AAGATGGCTTCTTCTGGGTGTTTCATTCGCGGATGACCTTGAAAGAGGAGACATGAC 681  
QY 221 MetPheThraspAnthrProleuglnasnlyrSerAsntrtpasnuglylnProser 240  
DB 682 ATGTCCACAGACAACTCCACTGCGAAGCTATAGCACTGAAATGACGGGAGACCCACAC 741  
QY 241 AspProTyrglyHlsaglyluspCysValglumetleuSerSerglyArgtrpAsntr 260  
DB 742 GACCCCTATGTCATAGACATGTGTGGAGATGCTGAGTCTGGCAGATGAGATGACACA 801  
QY 261 GluCysHlsleuthrmettyrPhevalCysglupheilelyslysllys 277  
DB 802 GAGTGCATCTTACCATGTACTTGTGTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 2  
US-09-978-697-96  
Sequence 96, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Askenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978, 697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11



PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	2,666-178	Length:	1016
Score:	1472.00	Matches:	275
Percent Similarity:	99.64%	Conservative:	1
Best Local Similarity:	99.28%	Mismatches:	1
Query Match:	99.19%	Indels:	0
DB:	9	Gaps:	0

US-09-600-932-2 (1-277) x US-09-978-697-96 (1-1016)

1 MetaAnglyPheAlaSerLeuAlaArgAsnGlnPheIleLeuValLeuPheLeu 20  
22 ATGAATGGCTTGGCTTCTTCTGCGAAGAAACCAATTATTCCTCTGCTATTTCTT 81  
21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
82 TTGCAATTCAGAGCTGGCTGTGATATGATAGCCCTCCACCGCTGAAGTCTGTGCC 141  
41 ThrHStrIleSerProGlyProGlyAspAspGlyGlyGlyAspProGlyGlu 60  
142 ACACACACAAATTCACCAAGACCCCAAGAGAGATGATGTGAAAAAGAGATCCAGAGAA 201  
61 GluGlyLysHsGlyLysValGlyArgMetGlyProGlyLysGlyLysGlyLysGly 80  
202 GAGGAGAAAGCATGGCAAGGTGGAGCATGGGGCCGAAAGAAATTAAGAGAACTGGGT 261  
81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyLysPlys 100  
262 GATATGAGAGATCAGAGCAATATGCAAGACTGGCCCATTTGGAGAAAGGTCGACAAA 321  
101 GlyLysGlyLysLeuGlyLysIleProGlyLysGlyLysAlaGlyThrValCysAsp 120  
322 GGGGAAAAAGCTTCTTCTGGAATACCTGAGAAAAAGCAAGCAGTCTGTCTGTAT 381  
121 CysGlyArgGlyArgLysPheValGlyLysLeuAspIleSerIleAlaArgLeuLysThr 140  
382 TGTGAAACATACCGGAAATTTGTTGCACTGATATATGCTGCGCTCAAGACA 441  
141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGluLysPheThr 160  
442 TCTATGAAGTTTGTCAAGATGTGTACAGAGGATTTAGGAAACTGAAAGAAATTTCTAC 501  
161 TyrIleValGlnGluLysAsnTyrArgLysSerLeuThrHsCysArgIleArgGly 180  
502 TACATCGTCAGAGAGAGAACTACAGGAACTCCCTAACCCACTGCAGATTCGGGGT 561  
181 GlyMetLeuAlaMetProLysAspGluAlaAsnThrIleAlaAspTyrValAla 200  
562 GGAATGCTAGCCATCCCAAGGATTAAGTCCCAACACATCCTGCTGATAGTTGCC 621  
201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
622 AAGAGAGGCTTCTTCTGCGGTTCATTGGCGGTGATGACCTTGAAGGAGGAGACAGTAC 681  
221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyLupros 240  
682 AAGTCCACAGACAACTCCACTGCAGAACTATACCACTGAAAGAGGAGGAGACCCAGC 741  
241 AspProTyrGlyHsGlyLysAspCysValGluMetLysSerSerGlyArgTyrAsnAsp 260  
742 GACCCCTATGATGATGAGAGACTGTGTGAGATGCTGAGCTCTGGAGATGGAATGACACA 801  
261 GluCysHsLeuThrMetLysPheValCysGluPheIleLysLysLys 277  
802 GAGTGCACATCTACCATGATCTTGTCTGTGAGTTCATCAGAAAGAAAAAG 852

RESULT 3

US-09-978-192A-96  
Sequence 96, Application US/09978192A  
Patent No. US2002017753A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
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APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2,66e-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.648 Conservative: 1  
Best Local Similarity: 99.288 Mismatches: 1  
Query Match: 99.198 Indels: 0  
DB: 9 Gaps: 0

US-09-600-932-2 (1-277) x US-09-978-192A-96 (1-1016)

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Db 22 ATGAATGCTTTCATCCCTGCTGAGAAACCAATTATCTCTGCTGCTATTTCTT 81  
QY 21 LeuGInIleGInSerLeuNgLyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
Db 82 TTGCAATTCAGAGTCTGGGCTGTGATATTGTATACCGCTACCGCTGAGAGTGTGACC 141

QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluLysGlyAspProGlyGlu 60  
|||||  
Db 142 ACACACACATTTCCACGACGACCAAGAGATGATGAGAAAGAGATCCAGAGAA 201  
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyLysLysGlyLysGly 80  
|||||  
Db 202 GAGGGAAGAGATGAGCAAGTGGGACCATGGGCGCCAAAGAAATTAAGAGAGAACTGGGT 261  
QY 81 AspMetGlyLysPargLysAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100  
|||||  
Db 262 GATATGGAGATGAGGCAATATGGCAAGACTGGGCGCCATGGGAGAGAGGTGCAAA 321  
QY 101 GlyLysGlyLysLeuGlyLysLeuGlyLysProGlyGlyLysGlyLysLysValGlyAsp 120  
|||||  
Db 322 GGGGAAAAAGGTTTGGCTGGAAATACCTGGGAAAAAGGCAAGAGAGTCTGCTGTAT 381  
QY 121 CysGlyArgGlyArgGlyPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140  
|||||  
Db 382 TGTGGAAGATACCGGAATTTGTTGACCACTGGAAATTAATTTGCTGGCTCAAGACA 441  
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyLysGlyLysGlyPheArg 160  
|||||  
Db 442 TCTATGAGAGTTTGTCAAGATGATGATGACGAGGATTAAGGAAACTGAGAGAAATTTCTAC 501  
QY 161 TyrIleValGlnGluLysAsnTyrArgGlySerLeuThrHisCysArgIleArgGly 180  
|||||  
Db 502 TACTCTCTGACGAGAGAGAACTACAGGGAATCCCTAACCCACGACGAGATTCGGGT 561  
QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaSerThrLeuIleAlaSerPyrValAla 200  
|||||  
Db 562 GGAATGCTACCTTCCCAAGATGATGATGACGAGGATTCCTGCTGCTGTGTGCTG 621  
QY 201 LysSerGlyPhePheArgValPheIleGlyValAspAspLeuArgGluGlyGlnTyr 220  
|||||  
Db 622 AAGAGTGGCTTTCTTGGGTGTTCAATGGGCTGAATGACCTGAAAGGAGGAGGAGCTAC 681  
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrAsnGluGlyProSer 240  
|||||  
Db 682 ATGCCCAACAGACACTCCACGACGAGACTATAGCACTGGAATGAGGGGAGAACCCAC 741  
QY 241 AspProTyrGlyHisGlyAspCysValGluMetLeuSerSerGlyArgTyrAsnAspThr 260  
|||||  
Db 742 GACCCCATGCTATGAGGACTGTGAGAGATCTAGCTGCTGCGCAGATGAGATGACAA 801  
QY 261 GluGlyHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277  
|||||  
Db 802 GAGTGGCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

## RESULT 4

US-09-999-832A-96

Sequence 96, Application US/09999832A

Publication No. US20020192706A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC63  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
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PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-08  
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PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
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PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
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PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639

PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 2,66e-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.64% Conservative: 1  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 99.19% Indels: 0  
DB: 9 Gaps: 0

US-09-600-932-2 (1-277) x US-09-999-832A-96 (1-1016)

QY 1 MetasnnglyphealaserleuargnsnglnbhelreuleuValleupheleu 20  
DB 22 ATGAATGCTTGCACTTCCTTCGAGAAACCAATTATCCCTGGTACTATTCTT 81  
QY 21 LeuglnlelnserleuglyleuaspilleaspearatprothralagluValcysala 40  
DB 82 TTGCAATTCAGAGCTGGGCTCGATATGATGCCGTCTACCGCTGAAGTCTGCC 141  
QY 41 ThrHstHrllleserproglyprolysglyaspaspelgylulysgilyaspProglyglu 60  
DB 142 ACACACACAAATTCACCGACGCCAACCAAGAGATGATGTGAAAAAGAGATCCAGGAGAA 201  
QY 61 Gluglylyshisgilylyvalglyargmetcylprolysgilylelysgilylulegly 80  
DB 202 GAGGGAAGCATGGCAAAAGTGGACGATGGGCGCAAGAAATTAAGAGAACTGGGT 261  
QY 81 AspmetglyaspargglyasnilleglylysthyProilleglylylysglyaspLys 100  
DB 262 GATATGGAGATCCAGGCAATATTTGGCAAGCTGGCCCATTTGGAGAAAGGCGACAAA 321  
QY 101 GlylulysgilyleuLeuglylleProglyglululysgilylsalaglyThrValcysasp 120  
DB 322 GGGGAAAAAGTTTGCTTGATACCTCGGAGAAAAAGCAAGAGCTACTGTCTGTGAT 381  
QY 121 CysgllyarglytraqglysphevalglylneuspilleserlleaIaargleuysThr 140  
DB 382 TGTGGAAGATCCCGCAATTTGTGTGCAACTGTGATTTGTGCTCGCTCAACACA 441  
QY 141 SermetlysphevallysasvalillealaglyllearggluThrIuglulyspHeTyr 160



Db 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGAGTTAGGAAGCTGAAGAAATTTCTAC 501  
QY 161 TTTTllevaGlnGlnGlnLysAsnTyrArgLysSerLeuThrHisCysArgIleArgly 180  
Db 502 TACATCGTGCAGAGAGAGAACTACAGGAAATCCCAACCCCTGACGATTCGGGGGT 561  
QY 181 GtmetLeuAlaMetProLysAspGluAlaIleAsnThrLeuIleAlaAspTyrValAla 200  
Db 562 GGAATGCTAGCCATCCCAAGAGATGACCTGCCAACACACATCCGCGATATGTTGCC 621  
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
Db 622 AAGAGTGGCTTCTTTCGGGGGTTCATGTGCGTGAATGACCTTGAAGGAGGACAGATAC 681  
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyProSer 240  
Db 682 ATGTCCACAGACACACTCCACTGCAGAACTATACCACTGATGAGGGGGAACCCAGC 741  
QY 241 AspProTyrGlyHisGluAspCysValGlnMetLeuSerSerGlyArgTyrPasnAspThr 260  
Db 742 GACCCCTATGCTCATGAGGAGACTGTGTGAGATGCTGAGACTGCGCAGATGGAATGACACA 801  
QY 261 GtucYshLsleuThrMetTyrPheValCysGluPheIleLysLysLys 277  
Db 802 GAGTGCATCTTACCATGACTTGTGTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 5  
US-09-978-189-96  
Sequence 96, Application US/09978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kilavin, Iyar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
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PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
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PRIOR FILING DATE: 1998-03-26  
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PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/080165  
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PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
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PRIOR APPLICATION NUMBER: 60/081195  
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PRIOR FILING DATE: 1998-04-09  
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PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952



DB 802 GAGTGCATCTTACCATGTACTTGTCTGTCAGTTCATCAAGAAAAAG 852

RESULT 6

US-10-174-590-99

Sequence 99, Application US/10174590

Publication No. US2003008352A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey J.

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria K.

APPLICANT: Watanabe, Collin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C42

CURRENT APPLICATION NUMBER: US/10/174,590

CURRENT FILING DATE: 2002-06-18

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 99

LENGTH: 1016

TYPE: DNA

ORGANISM: Homo Sapien

US-10-174-590-99

Alignment Scores:

Pred. No.: 2,66e-178 Length: 1016

Score: 1472.00 Matches: 275

Percent Similarity: 99.64% Conservative: 1

Best Local Similarity: 99.28% Mismatches: 1

Query Match: 99.19% Indels: 0

Gaps: 0

DB: 9

US-09-600-932-2 (1-277) x US-10-174-590-99 (1-1016)

QY 1 MetAsnGlyPheAlaSerLeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeu 20

DB 22 ATGATGGCTTTCATCTTCTTCGAAAGAACCAATTATCCCTCGGACATCTTCTT 81

QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrIleAlaGlyValCysAla 40

DB 82 TTGCAATTCAGAGTCTGGGTCTGATATGATAGCCGCTCCTACCGCTGAAGTCTGGCC 141

QY 41 ThrHisThrIleSerProGlyProGlyGlyAspAspGlyGlyGlyGlyGlyGlyGly 60

DB 142 ACACACACCAATTCACCGAGACCAAGACATATGATGAAAAAGAGATCCAGAGAA 201

QY 61 GluGlyIleGlyLeuGlyValGlyArgMetGlyProGlyGlyIleGlyGlyGlyGly 80

DB 202 GAGGGAAGCATGGCAAGGTGGAGCATGGGCGCAAGAAATTAAGAGAACTGGGT 261

QY 81 AspMetGlyAspArgGlyAsnIleGlyIleGlyThrGlyProIleGlyIleGlyAspGly 100

DB 262 GATATGGGAGATCAGGGCAATATGGCAAGACTGGGCCATGGGGAAGAGGGTACAAA 321

QY 101 GlyIleGlyGlyLeuLeuGlyIleProGlyGlyGlyGlyGlyGlyGlyGlyGly 120

DB 322 GGGGAAAAAGTTTGGCTTGGATACCTGGAGAAAAAGCAAGCAGGTACTGTGTGAT 381

QY 121 CysGlyArgGlyArgGlyPheValGlyGlnLeuAspIleSerIleAlaArgLeuGlyThr 140

DB 382 TGTGGAAATACCGGAAATTTGTGGACACTGGATATATATATGCTCGGCTCAAGACA 441

QY 141 SerMetGlyPheValGlyAsnValIleAlaGlyIleArgGlyIleGlyGlyGlyGly 160

DB 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAAGAACTGAAGCAATTTCTAC 501

QY 161 TyrIleValGlnGlnGlyIleAsnIleArgGlySerLeuThrHisCysArgIleArgGly 180

DB 502 TACATGTCAGAGGAAAGAAAGAACTACAGAGATCCCTAACCCACTGCGAGATCGGGGT 561

QY 181 GlyMetLeuAlaIleProGlyAspGlyValAlaAsnThrLeuIleAlaAspIleValAla 200

DB 562 GGAATGCTAGCCATGCGCAAGATGAGCTGCCAACACACTATCGCTACTATGTGGCC 621

QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlnArgGlyGlnIle 220

DB 622 AAGAGTGGCTTTCTTGGGTGTGATTCAGTGGCGTGAATGACCTTGAAGGAGGAGCAGTAC 681

QY 221 MetPheThrAspSerThrProLeuGlnAsnIleArgGlySerAsnIleAsnGlnIleGly 240

DB 682 ATGTCACAGACACACCTCCTCAGTACACTGACAACTGGAATGAGGGAGACCCAGC 741

QY 241 AspProGlyGlyHisGlnAspCysValGlnMetLeuSerSerGlyArgTrpAsnAspThr 260

DB 742 GACCCATAGGCATGATGAGATGCTGTGGAGATGCTGAGCTTGGCAGATGAGTACACA 801

QY 261 GluGlyHisLeuThrMetIlePheValCysGlnPheIleGlyGlyGlyGly 277

DB 802 GAGTGCATCTTACCATGTACTTGTCTGTCAGTTCATCAAGAAAAAG 852

RESULT 7

US-10-176-758-99

Sequence 99, Application US/10176758

Publication No. US2003008353A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey J.

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria K.

APPLICANT: Watanabe, Collin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C104

CURRENT APPLICATION NUMBER: US/10/176,758

CURRENT FILING DATE: 2002-06-21

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 99

LENGTH: 1016

TYPE: DNA

ORGANISM: Homo Sapien

US-10-176-758-99

Alignment Scores:

Pred. No.: 2,66e-178 Length: 1016

Score: 1472.00 Matches: 275

Percent Similarity: 99.64% Conservative: 1

Best Local Similarity: 99.28% Mismatches: 1

Query Match: 99.19% Indels: 0

Gaps: 0

DB: 9

US-09-600-932-2 (1-277) x US-10-176-758-99 (1-1016)

QY 1 MetAsnGlyPheAlaSerLeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeu 20

DB 22 ATGATGGCTTTCATCTTCTTCGAAAGAACCAATTATCCCTCGGACATCTTCTT 81

QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrIleAlaGlyValCysAla 40

DB 82 TTGCAATTCAGAGTCTGGGTCTGATATGATAGCCGCTCCTACCGCTGAAGTCTGGCC 141

QY 41 ThrHisThrIleSerProGlyProGlyGlyAspAspGlyGlyGlyGlyGlyGlyGly 60

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Db      142 ACACACACAAATTTACACAGACCCAAAGAGATATGTTAAAGAGATCCAGAGAA 201
QY      61  GLUGLYSHSLYSGLYSVALGVAIRMGELIPROLYSGLYILELYSGLYLUGLY 80
Db      202 GAGGGAAGAGCTTGCCAAAGTGGGACGATGGGCGGAAGAAATTTAAAGAGAACTGGGT 261
QY      81  ASPMETGLYASPARGLYSANILEGLYLYSTHRLGPROILEGLYLYSLYSGLYASPLYS 100
Db      262 GATATGGGAGATCAAGGCAATATTGGCAAGACTGGCCCATTTGGGAAGAGGGGTGACAAA 321
QY      101 GLYGLULYSGLYLAULEGLYILEPROGLYGLULYSGLYSLAAGLYTHRVALLCYASP 120
Db      322 GGGGAAAAAGTTTGCTTGGAATCTGGAGAAAAAGCAAGGCTACTGCTGTGAT 381
QY      121 CYSGLYARGLYTRARGLYSPHEVALGLYGLINLEUASPILESERILEALARGLEULYSTR 140
Db      382 TGTGGAAGATACCGGAATTTGTGGACAACTGGATTTAGTATGTGCTGGCTCAAGACA 441
QY      141 SERMETLYSPHEVALYSASNVALILEALAGLYLEARGGLUTHTGLUGLYLPHETRYR 160
Db      442 TCTATGAAGTTTGCAGAAATGTATAGCAGGATTTAGGAACTGGAAGAAATTTCTAC 501
QY      161 TYRILEVALINGLUGLYLUSASNTYRARGLUSERTLEUTHRLSCYSARGILEARGLY 180
Db      502 TACATCGTCAGAGAAAGAAAGAACTACAGGAATCCCTAACCCCTGACAGATTGGGGT 561
QY      181 GLYMETLEUALAMETPROLYSASPGLUALAALASANTHRLLEALASPTYRVALALA 200
Db      562 GGAATGCTAGCCATGCCCAAGATGAGAGTGCACACACTGATCGCTGATGTTGCC 621
QY      201 LYSSEIRGLYPHEPHEARVALPHEILEGLYVALASNAAPLEUGLUAGGLUGLYLTYR 220
Db      622 AAGAGTGGCTTCTTTCGGGTCTTCAATGCGCTGATGCTGAATGACCTTGAAAGGAGGACAGTAC 681
QY      221 METPHEIRHAPASANTHRLPROLEUGLNASNTYRSERANTPRASNGIUGLYLPROSER 240
Db      682 ATGTCCACAGACAAACACTCCACTGCAGAACTATAGCAACTGAGATGAGGGGAACCCAGC 741
QY      241 ASPPROTYRGLYHISGLYASPCYSVALGLUMETLEUSERSERGLYARGTPRASNAPTHR 260
Db      742 GACCCCTATGCTCAGAGACTGTGTGAGATGCTGAGCTGTGCAATGGAATGACACA 801
QY      261 GLUCYSHSLSEUTHRLMETLYRPHENALCYSGLUAPHEILELYSLYSLYS 277
Db      802 GAGTGCATCTTACCATGTACTTGTGCTGAGTTCAAGAAAGAAAG 852

```

# RESULT 8

```

; Sequence 99, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 99
; LENGTH: 1016
; TYPE: DNA

```

```

; ORGANISM: Homo Sapien
; US-10-175-737-99
Alignment Scores:
Pred. No.: 2,666-178
Score: 1472.00
Percent Similarity: 99.64%
Best Local Similarity: 99.28%
Query Match: 99.19%
DB: 9
Gaps: 0
US-09-600-932-2 (1-277) x US-10-175-737-99 (1-1016)
QY      1  METASNGLYPHEALASERLEUARGARGASNGINPHEILELEUENVALLEUPHELEU 20
Db      22  ATGAATGCTTGTCATCTTCTGTCGAAGAAACCAATTTATCTCTGCTACTATTCTT 81
QY      21  LEUGLILEGLSERLEUGLYLEUASPILESERARARGPROTHRLAGLUVALCYSLA 40
Db      82  TTTCAATTCAGATGCTGGGTCTGATATTGATAGCCGCTTACCGCTGAATCTGTGCC 141
QY      41  THRISTHRLSESRPROGLYPROLYSGLYASPARGLYGLULYSGLYASPROGLYGLU 60
Db      142 ACACACACAAATTTACACAGACCCAAAGAGATGATGTTGGAAGAAAGAGATCCAGAGAA 201
QY      61  GLUGLYSHSLYSGLYVALGVAIRMGELIPROLYSGLYILELYSGLYLUGLY 80
Db      202 GAGGGAAGAGCTTGCCAAAGTGGGACGATGGGCGGAAGAAATTTAAAGAGAACTGGGT 261
QY      81  ASPMETGLYASPARGLYSANILEGLYLYSTHRLGPROILEGLYLYSLYSGLYASPLYS 100
Db      262 GATATGGGAGATCAAGGCAATTTGGCAAGACTGGGCCATTTGGGAAGAGGTTGACAAA 321
QY      101 GLYGLULYSGLYLAULEGLYILEPROGLYGLULYSGLYSLAAGLYTHRVALLCYASP 120
Db      322 GGGGAAAAAGTTTGCTTGGAATCTGGAGTACCTGGAGAAAAAGCAAGGATGCTGTGAT 381
QY      121 CYSGLYARGLYTRARGLYSPHEVALGLYGLINLEUASPILESERILEALARGLEULYSTR 140
Db      382 TGTGGAAGATACCGGAATTTGTGGACAACTGGAATTTAGTATGTGCTGCTCAAGACA 441
QY      141 SERMETLYSPHEVALYSASNVALILEALAGLYLEARGGLUTHTGLUGLYLPHETRYR 160
Db      442 TCTATGAAGTTTGCAGAAATGTATAGCAGGATTTAGGAAACCTGGAAGAAATTTCTAC 501
QY      161 TYRILEVALINGLUGLYLUSASNTYRARGLUSERTLEUTHRLSCYSARGILEARGLY 180
Db      502 TACATCGTCAGAGAAAGAAAGAACTACAGGAATCCCTAACCCCTGACAGATTGGGGT 561
QY      181 GLYMETLEUALAMETPROLYSASPGLUALAALASANTHRLLEALASPTYRVALALA 200
Db      562 GGAATGCTAGCCATGCCCAAGATGAGAGTGCACACACTGATCGCTGATGTTGCC 621
QY      201 LYSSEIRGLYPHEPHEARVALPHEILEGLYVALASNAAPLEUGLUAGGLUGLYLTYR 220
Db      622 AAGAGTGGCTTCTTTCGGGTCTTCAATGCGCTGATGCTGGAATGACCTTGAAAGGAGGACAGTAC 681
QY      221 METPHEIRHAPASANTHRLPROLEUGLNASNTYRSERANTPRASNGIUGLYLPROSER 240
Db      682 ATGTCCACAGACAAACACTCCACTGCAGAACTATAGCAACTGAGATGAGGGGAACCCAGC 741
QY      241 ASPPROTYRGLYHISGLYASPCYSVALGLUMETLEUSERSERGLYARGTPRASNAPTHR 260
Db      742 GACCCCTATGCTCAGAGACTGTGTGAGATGCTGAGCTGTGCAATGGAATGACACA 801
QY      261 GLUCYSHSLSEUTHRLMETLYRPHENALCYSGLUAPHEILELYSLYSLYS 277
Db      802 GAGTGCATCTTACCATGTACTTGTGCTGAGTTCAAGAAAGAAAG 852

```

## RESULT 9

```

; Sequence 99, Application US/10173706
; Publication No. US20030022283A1

```

```

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C7
CURRENT APPLICATION NUMBER: US/10/173,706
PRIORITY FILING DATE: 2002-06-17
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 99
LENGTH: 1016
TYPE: DNA
ORGANISM: Homo Sapien
US-10-173-706-99

Alignment Scores:
Pred. No.: 2,666-178 Length: 1016
Score: 1472.00 Matches: 275
Percent Similarity: 99.64% Conservative: 1
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 99.19% Indels: 0
DB: Gaps: 0

US-09-600-932-2 (1-277) x US-10-173-706-99 (1-1016)
QY 1 MetasnGLYPheAlaserLeuArGArGsnGlnPheIleLeuValLeuPheLeu 20
DB 22 ATGATAGCTTTCATCTCTGCTGAGAAACCAATTATCTCTGCTGCTATTTCTT 81
QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40
DB 82 TTGCAATTCAGAGCTGCTGCTGATTTGATGATGACCCGCTGACGCTGAAGTCTGTC 141
QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluValGlyAspProGlyGlu 60
DB 142 ACACACACAAATTCACAGACCCCAAGAGATGATGAGAAAGAGATCCAGAGAGA 201
QY 61 GluGlyLysHisGlyLysValGlyValGlyMetGlyProLysGlyIleLysGlyGluLeuGly 80
DB 202 GAGGGAAGACATGGCAAGTGGAGCCATGGGCGCAAGATTAAGAGAGAACTGGGT 261
QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysLysGlyAspLys 100
DB 262 GATATGGAGATCAGGCAATATGCGCAAGACTGGGCCCATTTGGAGAGAGGAGTGACAAA 321
QY 101 GlyGlyLysGlyLeuLeuGlyIleProGlyGlyLysGlyLysAlaGlyThrValCysAsp 120
DB 322 GGGGAAAAAGTTTGGTTCGATACCTGGAGAAAAAGCAAGCAAGCTCTGTGTGAT 381
QY 121 CysGlyArgTyrArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140
DB 382 TGTGGAAGATACCGCAATTTGTTGGCAACAGATGATATGATGCTGCGCTCAAGACA 441
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGlnGluLysPheTyr 160
DB 442 TCTATGAAAGTTTGTCAAGATGATGATGAGGATGAGGAAGCAAGCAAGAAATTCAC 501
QY 161 TyrIleValGlnGluLysAsnTyrArgLysLeuThrHisCysArgIleArgGly 180
DB 502 TACATGCTGCGAGAGAGAGAACTACAGGAAATCCCTAACCACTGCGAGATGGGGT 561
QY 181 GlyMetLeuAlaMetProLysAspGluAlaIleAsnThrLeuIleAlaAspTyrValAla 200

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DB 562 GGAATGCTAGCCATGCCCAAGAGATGAGCTCCCAACACTCATCGTGAATGTTGCC 621
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGluGlnTyr 220
DB 622 AAGATGGCTTCCTTCGGGTGCTCATGCGGTGATGACCTTAAGAGGAGGAGCAAGTAC 681
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAspThrAsnGlnGlyIleProSer 240
DB 682 ATGTCCACAGACACTCCACTGCACAGACTATGCACTGAGATGAGAGGGGAAACCCAGC 741
QY 241 AspProTyrGlyHisGluAspCysValGluMetLeuSerSerGlyArgTyrAsnAspThr 260
DB 742 GACCCCTATGCTCATGAGACTGCTGAGAGATGCTGAGCTGCGACAGATGAGATGACACA 801
QY 261 GluGlyHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277
DB 802 GAGTGCACTCTTACCATGATGATCTTGTGTGAGTTCATCAAGAGAAAG 852

RESULT 10
US-10-175-738-99
Sequence 99, Application US/10175738
Publication No. US20030022294A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C45
CURRENT APPLICATION NUMBER: US/10/175,738
PRIORITY FILING DATE: 2002-06-19
Prior Application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 99
LENGTH: 1016
TYPE: DNA
ORGANISM: Homo Sapien
US-10-175-738-99

Alignment Scores:
Pred. No.: 2,666-178 Length: 1016
Score: 1472.00 Matches: 275
Percent Similarity: 99.64% Conservative: 1
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 99.19% Indels: 0
DB: Gaps: 0

US-09-600-932-2 (1-277) x US-10-175-738-99 (1-1016)
QY 1 MetasnGLYPheAlaserLeuArGArGsnGlnPheIleLeuValLeuPheLeu 20
DB 22 ATGATAGCTTTCATCTCTGCTGAGAAACCAATTATCTCTGCTGCTATTTCTT 81
QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40
DB 82 TTGCAATTCAGAGCTGCTGCTGATTTGATGATGACCCGCTGACGCTGAAGTCTGTC 141
QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluValGlyAspProGlyGlu 60
DB 142 ACACACACAAATTCACAGACCCCAAGAGATGATGATGAGAAAGAGATCCAGAGAA 201
QY 61 GluGlyLysHisGlyLysValGlyValGlyMetGlyProLysGlyIleLysGlyGluLeuGly 80
DB 202 GAGGGAAGACATGGCAAGTGGAGCCATGGGCGCAAGATTAAGAGAGAACTGGGT 261

```

QY 81 AspmetGlyAspArgGlyAsnIleGlyThrGlyProIleGlyLysGlyAspLys 100  
 Db 262 GATATGGAGATCAGGAGCAATATGGCAAGCTGGGCCATTCGGAAGAAGGCTGACAA 321  
 QY 101 GlyGluGlyLeuLeuGlyIleProGlyGluGlyLysAlaGlyThrValCysAsp 120  
 Db 322 GGGGAAAAAGTTGCTGGTAATACCTGGGAAAAAGCAAAACAGGTACTGCTGTGAT 381  
 QY 121 CysGlyArgTyrArgLysPheValGlyIleLeuAspIleSerIleAlaArgLeuLysThr 140  
 Db 382 TGTGGAGATACCGGAAATTTGTGGACAACTGGATATAGTATTCCTCGGCCCAAGACA 441  
 QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGluGlyLysPheTyr 160  
 Db 442 TCTATGAGATTGTCCAGAAATGTGATAGCAGGATAGGAAACTGAAAGAAATTTCTAC 501  
 QY 161 TyrIleValGlnGluGlyLysAsnTyrArgGlySerLeuThrHisCysArgIleArgGly 180  
 Db 502 TACATCGTCGAGAGAGAAAGAACTACAGGAAATCCCTAACCCACTGCAGATTCGGGT 561  
 QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
 Db 562 GGAATGCTACCAATGCCCAAGATGAGAGCTGCCCAACACTCATCCCTGACTATGTTGCC 621  
 QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
 Db 622 AAGAGTGGCTTTCTTGGGTGTTCATTTGGCTGAATGACCTGAAAGGAGGACAGTAC 681  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyProSer 240  
 Db 682 ATGCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCACAC 741  
 QY 241 AspProTyrGlyHisGlyAspCysValGluMetLeuSerSerGlyArgTyrPasnAspThr 260  
 Db 742 GACCCCATGTGATGAGAGCTGTGTGAGATGCTGAGCTGCGCAGATGAGATGACACA 801  
 QY 261 GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277  
 Db 802 GAGTGCATCTTACCAATGCTGTGTCTGTGAGTTCATCAAGAAAGAAAAAG 852

## RESULT 11

US-10-175-752-99  
 ; Sequence 99, Application US/10175752  
 ; Publication No. US20030022295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Matanabe, Collin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zhen  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C60  
 ; CURRENT APPLICATION NUMBER: US/10/175,752  
 ; PRIORITY FILING DATE: 2002-06-19  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 99  
 ; LENGTH: 1016  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-175-752-99

Alignment Scores:  
 Pred. No.: 2,666-178 Length: 1016  
 Score: 1472.00 Matches: 275  
 Percent Similarity: 99.64% Conservative: 1

Best Local Similarity: 99.28% Mismatches: 1  
 Query Match: 99.19% Indels: 0  
 DB: 9 Gaps: 0

US-09-600-932-2 (1-277) x US-10-175-752-99 (1-1016)

QY 1 MetAsnGlyPheAlaSerLeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeu 20  
 Db 22 ATGAATGGCTTTCGATCTCTGCTCGAAGAAACCAATTAATCCCTCGGTACTTCTTCT 81  
 QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
 Db 82 TTGCAAAATTCAGAGCTGGTCTGTGATATTAATAGCCCTCTACCGCTGGAAGTGTGCC 141  
 QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyGluGlyLysGlyAspProGlyGlu 60  
 Db 142 ACACACACAAATTTCCAGCAGAACCCAAAGCAATATGATGTGAAAAAGAGATCCAGAGAA 201  
 QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyGluLeuGly 80  
 Db 202 GAGGGAAGACATGGCAAGTGGAGCGCATGGGGCGGAAAGAAATTAAGAGAACTGGCT 261  
 QY 81 AspmetGlyAspArgGlyAsnIleGlyThrGlyProIleGlyLysGlyAspLys 100  
 Db 262 GATATGGAGATCAGGAGCAATATGGCAAGCTGGGCCATTCGGAAGAAGGCTGACAA 321  
 QY 101 GlyGluGlyLeuLeuGlyIleProGlyGluGlyLysAlaGlyThrValCysAsp 120  
 Db 322 GGGGAAAAAGTTGCTGGTAATACCTGGGAAAAAGCAAAACAGGTACTGCTGTGAT 381  
 QY 121 CysGlyArgTyrArgLysPheValGlyIleLeuAspIleSerIleAlaArgLeuLysThr 140  
 Db 382 TGTGGAGATACCGGAAATTTGTGGACAACTGGATATAGTATTCCTCGGCCCAAGACA 441  
 QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGluGlyLysPheTyr 160  
 Db 442 TCTATGAGATTGTCCAGAAATGTGATAGCAGGATAGGAAACTGGAATGAGGGGGAACCCACAC 501  
 QY 161 TyrIleValGlnGluGlyLysAsnTyrArgGlySerLeuThrHisCysArgIleArgGly 180  
 Db 502 TACATCGTCGAGAGAGAAAGAACTACAGGAAATCCCTAACCCACTGCAGATTCGGGT 561  
 QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
 Db 562 GGAATGCTACCAATGCCCAAGATGAGAGCTGCCCAACACTCATCCCTGACTATGTTGCC 621  
 QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
 Db 622 AAGAGTGGCTTTCTTGGGTGTTCATTTGGCTGAATGACCTGAAAGGAGGACAGTAC 681  
 QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGluGlyProSer 240  
 Db 682 ATGCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCACAC 741  
 QY 241 AspProTyrGlyHisGlyAspCysValGluMetLeuSerSerGlyArgTyrPasnAspThr 260  
 Db 742 GACCCCATGTGATGAGAGCTGTGTGAGATGCTGAGCTGCGCAGATGAGATGACACA 801  
 QY 261 GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277  
 Db 802 GAGTGCATCTTACCAATGCTGTGTCTGTGAGTTCATCAAGAAAGAAAAAG 852

## RESULT 12

US-10-176-482-99  
 ; Sequence 99, Application US/10176482  
 ; Publication No. US20030022295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.



```

QY 121 CysGlyArgTyrArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140
DB 382 TGTGGAAATACCGGAATTTGTGGCAACACTGGAATATATGCTGGCTCAACACA 441
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgLysThrGlnLysPheThr 160
DB 442 TCTATGAAGTTGTTCACAAATGTGATAGCAGGATTTAGGAACTGAAGAATTTCTAC 501
QY 161 TyrIleValGlnGlnGlnLysAsnTyrArgLysLeuThrHisCysArgIleArgGly 180
DB 502 TACATCGTCGAGGAAGAGAACTACAGGGAATCCCTAACCCACTCAGGATTCGGGGT 561
QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200
DB 562 GGAATGTAGCCATCCCAAGAGATGAACTGCCAACACACTCATCGCTAGCTATGTTGCC 621
QY 201 LysSerGlyPhePheArgValAlaPheIleGlyValAsnAspLeuGlnArgGlyGlnTyr 220
DB 622 AAGAGTGGCTCTTCTGGGGTGTATGCGTGAATGACCTTGAAGGAGGACAGTAC 681
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGlnGlyLupProSer 240
DB 682 ATGTCCACAGACAAACACTCCACTGACAGACTATAGCAACTGTGATGAGGGGAACTCCAGC 741
QY 241 AspProTyrGlyHisGluAspCysValGlnMetLeuSerSerGlyArgTyrPasnAspThr 260
DB 742 GACCCCTATGTGCATGAGAGACTGTGTGAGATGCTGAGCTGTGGCAGATGGAAGACACA 801
QY 261 GlucySHisLeuThrMetTyrPheValCysGlnPheIleLysLysLys 277
DB 802 GAGTGCCATCTTACCATGTACTTGTCTGTGAGTTCAACAGAAAGAAAAG 852

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RESULT 14
US-10-176-913-99
; Sequence 99, Application US/10176913
; Publication No. US2003002298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P343081C66
; CURRENT APPLICATION NUMBER: US/10/176,913
; PRIORITY FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 99
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-913-99

```

```

Alignment Scores:
Pred. No.: 2,66e-178 Length: 1016
Score: 1472.00 Matches: 275
Percent Similarity: 99.64% Conservative: 1
Best Local Similarity: 99.28% Mismatches: 1
Query Match: 99.19% Indels: 0
DB: 9 Gaps: 0

```

US-09-600-932-2 (1-277) x US-10-176-913-99 (1-1016)

QY 1 MetaAnglyPheAlaSerLeuThrArgLysGlnPheIleLeuValLeuPheLeu 20.

```

DB 22 ATCAATGGCTTTCATCTCTTGCATGAAACCACTTTATCTCTGCTGCTACTATTCTT 81
QY 21 LeuGlnIleGlnSerLeuGlnLysAsnIleAspSerArgProThrAlaGlnValCysAla 40
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGATATTTAGTACCGCTTCAACGCTCAATCTGTGCC 141
QY 41 ThrHisThrIleSerProGlyProLysGlyAspAspGlyLysGlyAspProGlyGly 60
DB 142 ACACACACATTTTCCACGAGACCCCAAGAGATGATGTGAAAAAGAGATCCAGAGAA 201
QY 61 GlnGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyLysLeuGly 80
DB 202 GAGGGAAGACATGGCAAAATGGGACCATGGGGCCCAAGCAATTAAGAGAACTGGGT 261
QY 81 AsnMetGlyAspArgLysAsnIleGlyLysThrGlnProIleGlyLysLysGlyAspLys 100
DB 262 GATATGGAGATCAGGCAATATTTGCAAGACTGGGCCCTTTGGAGAGAGGTGACAAA 321
QY 101 GlyLysLysGlyLeuLeuGlnIleProGlyGlnLysGlyLysAlaGlyThrValCysAsp 120
DB 322 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAAGCAAAAGCAAGTACTGTCTGTAT 381
QY 121 CysGlyArgTyrArgLysPheValGlyGlnLeuAspIleSerIleAlaArgLeuLysThr 140
DB 382 TGTGGAAGATACCGGAATTTGTGGACACTGGATATTAGTATGCTCGCTCAAGACA 441
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlnThrGlnLysPheThr 160
DB 442 TCTATGAAGTTTGTCAAGATGTGATGACAGGATTTAGGAAATGAAAGAAATTTCTAC 501
QY 161 TyrIleValGlnGlnGlnLysAsnTyrArgLysLeuThrHisCysArgIleArgGly 180
DB 502 TACATGCTGAGGAAGAAAGAACTACAGGATCCCTAACCCACTCAGGATTCGGGGT 561
QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200
DB 562 GGAATGTAGCCATCCCAAGAGATGAACTGCCAACACACTCATCGCTAGCTATGTTGCC 621
QY 201 LysSerGlyPhePheArgValAlaPheIleGlyValAsnAspLeuGlnArgGlyGlnTyr 220
DB 622 AAGAGTGGCTCTTCTGGGGTGTATGCGTGAATGACCTTGAAGGAGGACAGTAC 681
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPasnGlnGlyLupProSer 240
DB 682 ATGTCCACAGACAAACACTCCACTGACAGACTATAGCAACTGTGATGAGGGGAACTCCAGC 741
QY 241 AspProTyrGlyHisGluAspCysValGlnMetLeuSerSerGlyArgTyrPasnAspThr 260
DB 742 GACCCCTATGTGCATGAGAGACTGTGTGAGATGCTGAGCTGTGGCAGATGGAATGACACA 801
QY 261 GlucySHisLeuThrMetTyrPheValCysGlnPheIleLysLysLys 277
DB 802 GAGTGCCATCTTACCATGTACTTGTCTGTGAGTTCAACAGAAAGAAAAG 852

```

```

RESULT 15
US-10-180-552-99
; Sequence 99, Application US/10180552
; Publication No. US20030022300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

```



FILE REFERENCE: P3430R1C153  
CURRENT APPLICATION NUMBER: US/10/180.552  
CURRENT FILING DATE: 2002-06-25  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 99  
LENGTH: 1016  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-180-552-99

Alignment Scores:  
Pred. No.: 2,666-178 Length: 1016  
Score: 1472.00 Matches: 275  
Percent Similarity: 99.64% Conservative: 1  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 99.19% Indels: 0  
DB: Gaps: 0

US-09-600-932-2 (1-277) x US-10-180-552-99 (1-1016)

QY 1 MetAsnGlyPheAlaSerLeuLeuArgAsnGlnPheIleLeuValLeuPheLeu 20  
DB 22 ATGAATGCTTTCATCTTCTGCTGAGAGAACCAATTATCTCTGCTGCTTCTT 81  
QY 21 LeuGlnIleGlnSerLeuGlyLeuAspIleAspSerArgProThrAlaGluValCysAla 40  
DB 82 TTGCAAAATTCAGAGCTGGCTGGATATGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141  
QY 41 ThrHisThrIleSerProGlyProGlyAspAspGlyGluValGlyAspProGlyGlu 60  
DB 142 ACACACACAAATTTCCACGAGACCCAAAGAGATGATGTGTAAGAGATCCAGAGAA 201  
QY 61 GluGlyLysHisGlyLysValGlyArgMetGlyProLysGlyIleLysGlyLeuGly 80  
DB 202 GAGGAGAAAGCATGGCAAAAGTGGAGCATGGGCGCGAAGAAATTAAGAGAACTGGCT 261  
QY 81 AspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyAspLys 100  
DB 262 GATATGGGAGATCAAGGCAATATGGCAAGCTGGCCCATGGCAAGAGAGGCTGACAAA 321  
QY 101 GlyGluLysGlyLeuLeuGlyIleProGlyLysGlyLysAlaGlyThrValCysAsp 120  
DB 322 GGGGAAAAAGTTTCTCTGGAATACCTGAGAAAAAGCAAGCAAGTCTGTCTGTAT 381  
QY 121 CysGlyArgGlyArgLysPheValGlyLysLeuAspIleSerIleAlaArgLeuLysThr 140  
DB 382 TGTGAAAGATACCGGAAATTTGTTGACACTGATATTGCTCGGCTCAGACA 441  
QY 141 SerMetLysPheValLysAsnValIleAlaGlyIleArgGlyThrGluGlyLysPheThr 160  
DB 442 TCTATGAAGTTGTCAAGATGTGTAGCAGGAGATTAGGAACTGAGAGAGAAATTTCTAC 501  
QY 161 TyrIleValGlnGluLysAsnTyrArgGluSerLeuThrHisCysArgIleArgGly 180  
DB 502 TACATCGTCAGAGAGAGAACTACAGGAACTCCCTAACCACTGCAGATTCGGGGCT 561  
QY 181 GlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyrValAla 200  
DB 562 GGAATGCTAGCCATGCCAAGAGTGAAGTGAACACACATCCTGCTGACTATGTTGCC 621  
QY 201 LysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGlyGlnTyr 220  
DB 622 AAGATGGCTTCTTTCGGGTGTTCAATGGCGTGAATGACCTTGAAAGGAGAGGACAGTAC 681  
QY 221 MetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnTyrPheAsnGluGlyProSer 240  
DB 682 ATGTCCACAGACAACTCCACTGACAACTATAGCACTGGAATGAGGGGAGACCCAGC 741  
QY 241 AspProTyrGlyHisGlyLysAspCysValGluMetLeuSerSerGlyArgTyrPheAsnAspThr 260  
DB 742 GACCCCTATGTCATAGAGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801

QY 261 GluCysHisLeuThrMetTyrPheValCysGluPheIleLysLysLysLys 277  
DB 802 GAGTGCATCTTACCAATGATCTTGTGTGAGTTGATCAAGAGAAAAAG 852

Search completed: June 15, 2003, 08:45:54  
Job time : 160 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 15, 2003, 05:56:57 ; Search time 1425 Seconds

(without alignments)  
3148.175 Million cell updates/sec

Title: US-09-600-932-2

Perfect score: 1484

Sequence: 1 MNGFASLRNMQFILLVFL.....NDTECHLMTFVCEFKKK 277

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL-frame\_plus\_p2n.model -DEV-xip  
-Q/cgn2\_1/USPTO\_pool/US09600933/1unat\_09062003\_094531\_25993/app\_query.fasta.1.455  
-DB-EST -QFMT-fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=100 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE-LOCAL  
-OUTFMT=ptc -NORM-ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09600933@cgn2\_1.1535 -unat\_09062003\_094531\_25993 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGEDEV -NEG\_SCORE=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1215	81.9	752	13	BM009998 603630745
2	917	31.8	955	13	BB612129
3	782	52.7	609	13	BM010788
4	777	52.4	482	12	BF078010
5	731	49.3	489	13	BI67460
6	728	49.1	1383	11	AK003121
7	699.5	45.4	1426	11	BC009951
8	673	45.4	654	13	BI067078
9	611.5	41.2	451	14	BO927000
10	596	40.2	451	10	AM355638
11	547	36.9	380	10	BB869893
12	538	36.3	893	12	BF314316
13	532	35.8	361	10	BB869996
14	532	35.8	486	13	BM426695
15	517.5	34.9	823	13	BI198782
16	514	34.6	354	10	AM435866
17	505	34.0	962	14	BO069775
18	477	32.1	788	12	BF311981
19	474	31.9	723	10	BE382845
20	462	31.1	1239	13	BM551435
21	456	30.7	1012	10	BE260904
22	454.5	30.6	640	10	BE383325
23	453.5	30.6	672	12	BF206254
24	445.5	28.9	702	12	BF311185
25	444	28.9	1094	13	BM577424
26	441	29.7	590	10	AV690347
27	429	28.9	683	10	BE382433
28	426	28.7	326	14	R29493
29	421.5	28.4	644	10	BE262656
30	417.5	28.1	715	10	BE313199
31	414.5	27.9	737	10	BE313410
32	412	27.8	916	12	BF316777
33	411.2	27.7	564	9	AI353438
34	409.5	27.6	626	12	BF316436
35	403.5	27.2	613	12	BF312666
36	401.5	27.1	654	10	BE312923
37	400.5	27.0	767	10	BE260355
38	395	26.6	728	10	BE260359
39	388.5	26.2	892	12	BF314275
40	388	26.1	602	13	BI442205
41	384.5	25.9	1000	13	BI198831
42	378	25.5	362	14	R97480
43	376.5	25.4	538	10	BE312003
44	369.5	24.9	619	13	BI199068
45	369	24.9	697	12	BF317087

ALIGNMENTS

RESULT 1  
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LOCUS 603630745F1 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5444459 5',  
DEFINITION mRNA sequence.  
ACCESSION BM009998  
VERSION BM009998.1 GI:16524352  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (Bases 1 to 752)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)



**source**

```

source
1. 955
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4432404008"
/liver=""
/sex="mixed"
/tissue_type="liver"
/dev_stage="14 days embryo"
/lab_host="DH10B"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGAGATCCAGACGCTCTTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGAGATTCGAGGTATTAATTAATCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pbluescript KS(+) after bulk excision from Lambda PUC I"
264 a 180 c 261 g 249 t 1 others

```

BASE COUNT	264 a	180 c	261 g	249 t	1 others
ORIGIN					

**Alignment Scores:**

Pred. NO.:	1.02e-93	Length:	955
Score:	917.00	Matches:	204
Percent Similarity:	80.73%	Conservative:	18
Best Local Similarity:	74.18%	Mismatches:	48
Query Match:	61.79%	Indels:	12
DB:	10	Gaps:	3

US-09-600-932-2 (1-277) x BB612129 (1-955)

QY	1	MetansnglyPhealaserleuAlyArgysnlnPheileuValleuPheleu	20
Db	9	ATGATAGGCTTTAAAGTCCTCTCGAAGCAACCTACCATCGCTGTGCTAGCTCTC	68
QY	21	LeuGlnilegInserleuGlyleuAspIleAspSerArgProthrAlaGluValCysAla	40
Db	69	TTGCACCTTTCAGAGTCTGGGCTCTGGATGGTGTATGTAGTCAGTCGCAAGAGTCTGGCC	128
QY	41	ThrIsthrIleSerProGlyProIlyGlyAspAspGlyGlyAspProGlyGlu	60
Db	129	ACACATCCCATTTTACCAAGACCTAAAGGGGATATGTGTAAAGAGGTGACACAGAGAA	188
QY	61	GluGlyIysHIsGlyIysValGlyArgMetGlyProIlyGlyIleIysGlyIleuGly	80
Db	189	GAAAGCAAGATGGCAAAAGTGGAGCAGCCAGGACCAAAAGAGAGGAAAGAGACTGGCT	248
QY	81	AspMetGlyAspArgGlyAsnIleGlyIysThrGlyProIleGlyIysGlyAspIys	100
Db	249	GATATGGGAGGCCGGGGTAAATATTGGCAAGCTGCGCCCTATTGGCAAGAGGGTGCAAAA	308
QY	101	GlyGlyIysGlyLeuIleuGlyIleAProGlyIuIysGlyIysAlaGlyThrValCysAsp	120
Db	309	GGGGAAAAAGGCTGCTGCTTGGAAATTCCTGGAGAAAAAGGCAAGCAGGTACCATCTGGAT	368
QY	121	CysGlyArgTyraGlySpheValGlyGluLeuAspIleSerIleAlaArgGlyLeuThr	140
Db	369	TGTGGCAGAGTCCCGAAAGTGGTGGACAACTGGATATTATGTGCTGCTGCTTAAGACA	428
QY	141	SerMetIysSpheValysAsnValIleAlaGlyIleArgIuThrGluIuGlyIysPheTyrr	160
Db	429	TCAATGAATTCATCAAGAAATGTTATATGACAGAGGATCCGGGAACTGGAAGAAATTTCTAC	488

QY	161	TyrIleValAlaGluGluGluGluAsnProTyrArgLysLeuSerLeuThrHisCysAsnArgIleArgGly	180
Db	489	TACATGTGCAGAGAGAGAGAAACATACAGGGAAATCTCGAACCCACCTCCAGATCCGAGGA	548
QY	181	GlyMetIleuAlaMetProLysAspGluIuaIaaIaaSnThrIleuIleIleAlaAspTyrValAla	200
Db	549	GGGATCTCGATGGCATGGTCAGAGATGAATCGCTGCACACCCCTAATGGTCACATGTGTGGC	608
QY	201	LysSerGlyPhePheArgValAlaPheIleGlyValAlaAsnAspLeuGluArgGluGlnTyr	220
Db	609	AG-AGGGGGTTC-AGAGTGTTCATATGGTGCAT-TACCTTAGAGAGGGGGG---CAT	662
QY	221	MetPheThrAspAsnThrProLeuGlnIaaSnTyrIleAsnTyrAsnArgIuGluProSer	240
Db	663	ATGTGCACAGATACATCTCCATTCAGAGAC-TACAGCAC-TGGAAAGAGAGAAACAT-AAT	719
QY	241	AspProTyrGlyHisGluAspCysValGluMetLeuSerGergIyArgTyrPheAsnAspThr	260
Db	720	GACCCATC-CGGCAGAGAGATGTGTGAAGACTGTGACTGTGAG-----AGGATGTGAC	768
QY	261	GluCysHisLeuThrMetTyrPheValGluGluPheIleLysIys	275
Db	769	CACATGTACCTTTTCA---TATTTTGTTTTGAGTTGTGAAGAAAAA	810
RESULT 3			
BM010788			
LOCUS	603693032FI NIH_MGC_41 Homo sapiens CDNA clone IMAGE:5434680 5',		
DEFINITION	MENA sequence.		
ACCESSION	BM010788		
VERSION	BM010788.1 GI:16525142		

REIMORDS  
SOURCE  
ORGANISM  
Hsi.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 609)  
NIN-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

**FEATURES**  
**SOURCE**

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5434680"
/clone_id="NH.MGC.41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pOTB1; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally clone into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH.MGC library."

```



JOURNAL  
COMMENT

EST discovery in swine  
Unpublished (2000)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithemail.marc.usda.gov  
Single pass sequencing. Bases called and alt. trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -mismatch 18  
and -mismatch 12 options.

## FEATURES

Source

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCAGCTCAGCAGC  
Plate: 142 row: E column: 10  
Seq primer: ATTATGGACACTATAG.

Location/Qualifiers

1..499  
/organism="Sus scrofa"  
/db\_xref="taxon:9823"  
/clone\_lib="MARC 2P10"  
/tissue\_type="pooled"  
/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
Library made from pooled tissue from testis, ovary,  
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 145 a 96 c 161 g 97 t

ORIGIN

## Alignment Scores:

Pred. No.: 6 38e-73 Length: 499  
Score: 731.00 Matches: 140  
Percent Similarity: 94.1% Conservative: 6  
Best Local Similarity: 90.32% Mismatches: 9  
Query Match: 49.26% Indels: 0  
DB: 13 Gaps: 0

US-09-600-932-2 (1-277) x B1467460 (1-499)

QY 1 Metnnglyphealaserleuauargrarnglnpheilleuauvalleupheleu 20  
DB 34 ATGGGTGGCTTGGAGCTGGAGCCCGAAGAAACAGTTCATCCCTCGGGGCTCTTCTT 93  
QY 21 Leuglnlleglnserleuglyleuaspilleaspearprothralagluvalcyala 40  
DB 94 TTGCAGATTCAGAGCTCGGTCTGACACACAGCTGCTACCCGTGAAGTCTGCCC 153  
QY 41 Thrhistrhileserproglyprolyaspaaspglylulysglyaspproglyglu 60  
DB 154 ACACACACAATTTCACCGACGACCAAGAGAGATGATGTGAAAAGAGATACAGAGAG 213  
QY 61 Gluglylyshlglylyvalaglyargmetglyprolyscglyllelysglyglulengly 80  
DB 214 GAGGGAAGCATGGAAAGTGAGGAGCTGGGGCCAAAAGAAATTAAGGGTGAAGTGGT 273  
QY 81 Aspmetglyasparglyasnrlglylythrlyprolleglylylysglyasplys 100  
DB 274 GATATAGAGAGACAGGAGCAACATGGCAGACCTGGCCCATTTGGCAAGAGGTGACAAA 333  
QY 101 Glyglylulysglyleuenglylleproglylulysglylysalaglythrvalcyasp 120  
DB 334 GGAGAAAAAGGGGTTCCCTCGGATGCTGGAGAAAAAGGCGAAGAGGTACTGCTGGAC 393  
QY 121 Cysglyatgtyrarglyphevalaglylnleuasplleserllealaargleuylethr 140  
DB 394 TCGGGAATATACCGGAAGGTGTGGACAACTGGATATACATGTGGCTCGCTGAAGACA 453  
QY 141 Sermetlysphevallyasnavallealaglylleargglunthr 155  
DB 454 TCGATGAAGTTTGTCAAGATGATATACAGAGGATTCGGGAACC 498

RESULT 6  
AK003121

## LOCUS

AK003121 1383 bp mRNA linear HNC 19-JAN-2002

## DEFINITION

Mus musculus adult male heart cDNA, RIKEN full-length enriched  
library, clone:1010001H16;homolog to COLLECTIN 34, full insert  
sequence.

## ACCESSION

AK003121 GI:12833583

## VERSION

HTC; CAP trapper.

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## AUTHORS

## TITLE

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## AUTHORS

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## MEDLINE

## PUBMED

## AUTHORS

## TITLE

## JOURNAL

1 Carninci, P. and Hayashizaki, Y.  
High efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap trapper selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159  
3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, S., Nishibe, T., Harada, A.,  
Tamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujikawa, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watabiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4 Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamazaki, I.,  
Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R.,  
Kadoya, K., Matsuda, H., Ashburner, M., Balci, S., Casavant, T.,  
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
Kuehl, P., Lewis, S., Matsuo, Y., Nakai, I., Pesole, G.,  
Quackenbush, J., Schriml, L. M., Staudli, F., Suzuki, R., Tomita, M.,  
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
Baldarelli, R., Barsh, G., Blake, J., Botfield, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bulc, C.,  
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
Marchionni, L., Mashima, J., Mazzarelli, J., Momberti, P., Nordone, P.,  
Rang, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
Toyo-oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.,  
Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851  
5 (bases 1 to 1383)  
Adachi, J., Aizawa, K., Akahira, S., Akinura, T., Aono, H., Arai, A.,  
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bulc, C.,  
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,  
Hara, A., Hayatsu, N., Hill, D., Hironaka, K., Hirokawa, T., Hori, F.,  
Hume, D., Imoto, K., Ishii, Y., Itoh, M., Iizawa, M., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Konno, H., Kondo, M., Koyama, S.,  
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,  
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,







## ORIGIN

Alignment Scores: 3,47e-66 Length: 654  
 Pred. No.: 673.00 Matches: 122  
 Score: 673.00 Conservative: 22  
 Percent Similarity: 83.72% Mismatches: 28  
 Best Local Similarity: 70.93% Indels: 0  
 Query Match: 45.35% Gaps: 0  
 DB: 13

US-09-600-932-2 (1-277) x B1067078 (1-654)

15 LeuValLeuPheLeuLeuGlnIleGlnSerLeuLeuAspIleAspSerPro 34  
 133 CTAGAGTGGCTTTCATCTCCAGTCCAGATTGTTGTTGATGTTGACATTCAGCT 192  
 35 ThrAlaGluValCysAlaThrHisThrIleSerProGlyProGlyAspAspGlyGlu 54  
 193 ACAACAGATGTCCTCTCCACACACATATTTTACCTGACCCAAAGGGGATGATGTGAA 252  
 55 LysGlyAspProGlyGluGluGlyHisGlyLysValGlyArgMetGlyProGlyGly 74  
 253 AAAGGAGATAGAGGAG 312  
 75 IleGlyGlyGluLeuGlyAspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIle 94  
 313 AACCAAG 372  
 95 GlyLysLysGlyAspLysGlyGluLysGlyLeuLeuGlyIleProGlyGlyLysGly 114  
 373 GGAG 432  
 115 AlaGlyThrValCysAspCysGlyArgGlyArgGlyAspValGlyGlnLeuAspIleSer 134  
 433 GCAGGACAGAGCTGTGACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492  
 135 IleAlaArgLeuLysThrSerMetLysPheValLysAsnValIleAlaGlyIleArgGlu 154  
 493 GTGTGCTGCTTAAACATCATCATCAAGTTTGTAAAGATGTATAGACAGCATCAGGAG 552  
 155 ThrGluGluLysPheTyrrTyrIleValGlnGluGluLysAsnTyrArgGluSerLeuThr 174  
 553 ACGGATGAGAAATCTCTATATATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612  
 175 HisCysArgIleArgGlyGlyMetLeuAlaMetPro 186  
 613 CATTCGNNNNNCAAGNNNNNCACTGGCCATGCT 648

RESULT 9  
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 LOCUS AGENCOURT 8804355 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6377965  
 DEFINITION 5' mRNA sequence.  
 ACCESSION BQ927000  
 VERSION BQ927000.1 GI:22342031  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 962)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: rgs@bbs-riemail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov

## FEATURES

Plate: L1CM2562 row: J column: 14  
 High quality sequence stop: 616.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone\_lib="NIH\_MGC\_47"  
 /tissue\_type="neuroblastoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: brain; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: This is a NIH\_MGC Library."

## BASE COUNT

203 a 275 c 323 g 157 t 4 others

## Alignment Scores:

Pred. No.: 5,42e-59 Length: 962  
 Score: 611.50 Matches: 120  
 Percent Similarity: 64.13% Conservative: 57  
 Best Local Similarity: 43.48% Mismatches: 86  
 Query Match: 41.21% Indels: 13  
 DB: 14 Gaps: 3

US-09-600-932-2 (1-277) x BQ927000 (1-962)

3 GlyPheAlaSerLeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeuGln 22  
 51 GGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 110  
 23 IleGlnSerLeuGlyLeuAspIleAspSerArgProThrAla-----GluValCys 39  
 111 CTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 170  
 40 AlaThrHisThrIleSerProGlyProGlyAspAspGlyGluGlyAspProGly 59  
 171 TCTGTGACAGATCT 224  
 60 GluGluGlyLysHisGlyLysValGlyArgMetGlyProGlyGlyIleLysGlyGlu 79  
 225 ---AAAGGCGCCCGGACGCGCTGAGAGAGTCGCGCCCGGAGGAGAGAGAGAGAG 281  
 80 GlyAspMetGlyAspArgGlyAsnIle-----GlyLysThrGlyProIleGlyLys 96  
 282 GGGGACAAAG 341  
 97 LysGlyAspLysGlyLysGlyLeuGlnIleProGlyGluGlyLysGlyValGly 116  
 342 AAAGGTGAGAGAGAGATTCGGGTGACATAGAGCCCGCTGCTTAATGAGAACAGAGC 401  
 117 ThrValCysAspCysGlyArgTyrArgLysPheValGlyGlnLeuAspIleSerIleAla 136  
 402 CTCCTCATGAG 461  
 137 ArgLeuLysThrSerMetLysPheValLysAsnValIleAlaGlyIleArgGluThrGlu 156  
 462 CAGCTACACAGCAGAGCTCAAGTTCATCAAGATGCTGTCGCGGTGTGGCAGACGGAG 521  
 157 GluLysPheTyrrTyrIleValGlnGluGluLysAsnTyrArgGluSerLeuThrHisCys 176  
 522 AGCAAGATCTACTGCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 581  
 177 ArgIleArgGlyLysLeuLeuAlaMetProLysAspGluAlaAlaAsnThrIleAla 196  
 582 CAGGCGCGGGGCGACGCTGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641  
 197 AspTyrValAlaLysSerGlyPhePheArgVal-PheIleGlyValAlaAspLeu--Glu 215





QY 190 AAlaAaenThrLeuileAlaAspTyrValAlaIysSerGlyPheArgValPheIle 209  
 DB 313 GCTGCATATGCGCCGATGAGCCGATACCTGCGCAAGCCGCGCCTGCGC-CGTGCTTATC 371  
 QY 210 GAlaValaAspLeuGluArgGluGlyGlnIleMetPheThrAspAsnThrProLeuGln 229  
 DB 372 GGCAATCAACGACGCTGAGAGAGAGGCGCCCTCGTGTACTGTGACACATCCCATCGG 431  
 QY 230 AsnIleSerAsnThrPaspGluGlyGluProSerAspProIleGlyHisGluAspCysVal 249  
 DB 432 ACCTTCAACAGATGCGCGAGCGGAGCCCAATGCTTACGAGAGAGAGAGAGAGAGAG 491  
 QY 250 GAluLeuSerSerGlyArgTyrPaspAspThrGluGlyHisLeuThrMetIleTyrPheVal 269  
 DB 492 GAGATGCTGCGCTGCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 550  
 QY 270 CysGluPhe 272  
 DB 551 TGTGAGTTT 559

RESULT 13  
 BB669996 361 bp mRNA linear EST 27-NOV-2001  
 LOCUS BB669996 RIKEN full-length enriched, adult male gall bladder Mus  
 DEFINITION musculus cDNA clone G630017H09 5', mRNA sequence.  
 ACCESSION BB669996  
 VERSION BB669996.1 GI:17116206  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 361)  
 Akimura, T., Aikawa, T., Carninci, P., Furuno, M., Hasegaki, T.,  
 Hayatsu, N., Hirose, K., Hirose, T., Hirose, T., Imotani, R., Ishii,  
 Y., Ito, M., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Matsuyama, T.,  
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,  
 Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,  
 Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa,  
 A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,  
 Watanabe, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.  
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.  
 2001)

TITLE Unpublished (2001)  
 CONTACT Yoshinobu Hayashizaki  
 LABORATORY for genome exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp,  
 url: http://genome.gsc.riken.go.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,  
 M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Itawa, M., Ohara, E.,  
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,  
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and  
 Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multichannel sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,  
 Y., and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.  
 e mouse tissues.

FEATURES  
 source location/Qualifiers  
 1. 361  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="G630017H09"  
 /clone\_lib="RIKEN full-length enriched, adult male gall  
 bladder"  
 /sex="male"  
 /tissue\_type="gall bladder"  
 /dev\_stage="adult"  
 /note="pooled tissues; (tissue\_type=cerebellum,  
 dev\_stage=16 days neonate, sex-mixed),  
 (tissue\_type=cerebellum, dev\_stage=0 day neonate,  
 sex-mixed), (tissue\_type=hippocampus, dev\_stage=adult,  
 sex-male), (tissue\_type=whole body, dev\_stage=9 days  
 embryo, sex-mixed), (tissue\_type=lung, dev\_stage=13 days  
 embryo, sex-mixed)"

BASE COUNT 103 a 67 c 117 g 74 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1,789-50 Length: 361  
 Score: 532.00 Matches: 98  
 Percent Similarity: 89.83% Conservative: 8  
 Best Local Similarity: 83.05% Mismatches: 12  
 Query Match: 35.85% Indels: 0  
 DB: 10 Gaps: 0

US-09-600-932-2 (1-277) x BB669996 (1-361)  
 QY 7 LeuLeuArgArgAsnGlnPheIleLeuValLeuPheLeuGlnIleGlnSerLeu 26  
 DB 8 CTCCTCGAAGCAACCTATCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 67  
 QY 27 GlyLeuAspIleAspSerArgProThrIleGluValCysAlaThrIleThrIleSerPro 46  
 DB 68 GGTCTGATGTTATATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 127  
 QY 47 GlyProIleGlyAspAspGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 66  
 DB 128 GGACCTAAAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 187  
 QY 67 ValGlyArgMetIleProIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 86  
 DB 188 GTGGAGCGCCAGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247  
 QY 87 AsnIleGlyIleThrGlyProIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 106  
 DB 248 AATATTGGCAAGCTGCGCTGATTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 307  
 QY 107 GlyIleProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 124  
 DB 308 GGAATTCCTGGAGAAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361

RESULT 14  
 BM426695 486 bp mRNA linear EST 30-JAN-2002  
 LOCUS BM426695 p6f2n.p6f2n.h13 Normalized Chicken Abdominal Fat Library (p6f2n)  
 DEFINITION Gallus gallus cDNA clone p6f2n.p6f2n.h13 5' similar to g1114741536  
 [ref1XP\_005080.3] collectin sub-family member 10 (C-type lectin)  
 [Homo sapiens], mRNA sequence.  
 ACCESSION BM426695  
 VERSION BM426695.1 GI:18431247  
 KEYWORDS EST.  
 SOURCE chicken.  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 486)  
 Cogburn, L.A., Morgan, R., and Burnside, J.  
 ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal

**JOURNAL  
COMMENT**

Genome Project  
Unpublished (2002)  
Contact: Larry A. Coghurn

## FEATURES

Email: cogburn@udel.edu, www.chickest.udel.edu  
Location/Qualifiers  
1. 486

BASE COUNT	170 a	78 c	134 g	102 t	2 others
ORIGIN					

Alignment Scores:

Pred. No.:	2,56e+50	Length:	466
Score:	532.00	Matches:	96
Percent Similarity:	83.82%	Conservative:	18
Best Local Similarity:	70.59%	Mismatches:	22
Query Match:	35.85%	Indels:	0
DB:	13	Gaps:	0

US-09-600-932-2 (1-277) X BM426695 (1-486)

OY		15	IleuLeuValIeuPheIeuLeuGluIleInserLeuGlyLeuAspIleAspSerArgPro	34
Dd		79	CTAGAGCGCTTTTCATCTTCCCAAGTTCACAGATTITGGTTTGATGTGGACAATCGACT	138
OY		35	ThrAlaGluValCysAlaThrHisThrIleSerProGlyProLysGlyAspAspGlyCys	54
Dd		139	AAACACAGTGTCTGTCTGCACACACACTATTTTACCCTGGACCCAAAAGGGGAAGATGGTGA	198
OY		55	LysGlyAspProGlyGluGluGlyLysHisGlyLysValGlyArgMetGlyProLysGly	74
Dd		199	AAGAAGATTAAGAGAGAGAGAGTGGCGAACACAGAAAGATTGGACCCAAAAGGACTTAAGGA	258
OY		75	IleLysGlyGluLeuGlyAspMetGlyAspArgGlyAsnIleGlyLysThrGlyProIle	94
Dd		259	AACAAAGAGACATGTGGGGATGTGCGTGATCCNMGAAATGCTGGGAAAAATGGGTCAATT	318
OY		95	GlyLysLysGlyAspLysGlyGluLysGlyLeuGlyLysIleProGlyLysGlyLys	114
Dd		319	GGAGGTAAAGGTGCACAAAGAGGCCAATAAGCATATCAGGGGGTGTCTGGAAAAAAGAGAAA	378
OY		115	AlaGlyThrValCysAspCysGlyArgTyrArgLysPheValGlyGlnLeuAspIleSer	134
Dd		379	GCAGGCACAGACTGTGACTGTGGAAAGTAGCGCAGAGTGTGGCACACTGAATATCAAT	438
OY		135	IleAlaArgLeuLysThrSerMetLysPheValLysAsnValIleAla	150
Dd		439	GTTGCTCGGCTTAACACATCATCAAGTTGTGAAGAAATGTTAATAGCA	486
RESULT 15				
Bil198782				
LOCUS	Bil198782	823 bp	mRNA	linear EST 10-JUL-2001
DEFINITION	602759811991 NTH_MGC_19 Homo sapiens cDNA clone IMAGEI:4895213 5'			
VERSION	Bil198782			
ACCESSION	Bil198782.1	GI:14653803		

**KEYWORDS**  
**SOURCE**  
**ORGANIZATION**

EST.  
human  
Homo

## ORGANIZATIONAL

**Homo sapiens**

## ORGANISM

**Homo sapiens**

## REFERENCE

1 (bases 1 to 823)

AUTHORS  
TITLE

National Institutes of Health. MGC  
NIH-MGC <http://mgc.ncl.nih.gov/>.

## JOURNAL

Unpublished (1999)

**COMMENT**

Contact: Robert Str

**COMMENT**

Contact: Robert Strausberg, Ph.D

Contact: Robert Strausberg,

Contact: Robert Strausberg,

Contact: Robert Strausberg,

Contact: Robert Strausberg,

Contact: Robert Strausberg,

Contact: Robert Strausberg,

Contact: Robert Strausberg,

Contact: Robert Strausberg,

## FEATURES

Location/Qualifiers

BASE COUNT	176 a	234 c	268 g	145 t
ORIGIN				

Alignment Scores:

Pred. No.:	823
Score:	517.50
Percent Similarity:	59.00%
Best Local Similarity:	40.61%
Query Match:	34.87%
DB:	13
Length:	106
Matches:	48
Conservative:	76
Mismatches:	31
Indels:	2
Gaps:	2

US-09-600-932-2 (1-277) x B1198782 (1-823)

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      111  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      49  GGRITCTCGCTCGCTCAGATGAGGGGAATCTGGCCCTGGTGGCGGTCTTAATACG  108
QY      23  ILeGInserLeuGlyLeuAspIleAspSerArgProThrAla-----GluValCys  39
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      109  CTGGCCCTCTGTGCACGTGTGCACATGTGCACATCTCTCAGCCGCGGATGAGCCCTGC  168
QY      40  AlArThrIshrIleSerProGlyProIlysgIyAspAparGlyIuIysgIyAspProGly  59
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      169  TCGTGCAGATCTCTGCTCCCTGGCCCTCAAAAGAGACATGGGGACAAAGACAAAGAGC  228
QY      60  GluGluGlyIyshIsgIyIyValGlyArgmetGlyProIlysgIyIleIyGlyIuLeu  79
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      229  AGTGTGGTGTGTATGAGAAAANT-----  255
QY      80  GlyAspmetGlyAspArgGlyAsnIleGlyIyThrGlyProIleGlyIyIyAsp  99
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      253  -----GGTCCCATGGCTCTAAAGAGTAG  278
QY      100  Lys-GLYGLuIyAsGlyLeuIleuGlyIleProGlyIuIyGlyIyIyAsIyAlaIyThrValCy  119
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      277  AACGGAGATTCGGGGACATAGAGACCCCTGTCTTAATGAGAACACAGGCTCCCATG  338
QY      119  sAspCysGlyArgTyArgIyAspValGlyIuIyGlnLeuAspIleSerIleAlaArgLeuLy  138

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Db 337 TGAGTGCAGCCAGCGCGCCAGAGGCGCATGCGGAGATGAGCAACACAGGTCCTCTCAGCTGAC 396
QY 139 sThSerMetLysPheValLysAsnValIleAlaGlyLeuArgLutHrGluLysPh 159
Db 397 CAGCGAGCTCAAGTTCATCAAGAAATGCTGCGCGGTGTGCGGAGAGAGAGCAAGAT 456
QY 159 eTyTrIleValGlnGluLysAsnTyArgGluSerLeuThrHisCysArgTLeAr 179
Db 457 CTACCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
QY 179 gGlyGlyMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIleAlaAspTyVa 199
Db 517 CGGGGGGACAGCTGAGACATGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
QY 199 lAlaLysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGluArgGluGly 219
Db 577 GCGCGAGAGCGCGCGCTGCGCGCGCTGCTTCATCGGCGCATCAAGAGAGAGAGAGAGAGAG 636
QY 219 nTyMetPheThr--AspAsnThrProLeuGlnAsnTySerAsnTyPasnGluGlyGlu 238
Db 637 CCTTGTGTAACCTGAGACCACTCCCGCATGCGAGACCTCAACAGAGTGCGGAGCGGTGAG 696
QY 239 -ProSerAspProTyArgLysHisGluAspCysValGluMetLeuSerSerGlyArg 256
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Search completed: June 15, 2003, 07:53:23  
Job time : 1432 secs

Qy 39 CysAlaThhIstHrIleSer-----ProGlyProLysGlyAspAsp-----Gly 53  
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QY 54 GLULYSGLYASPPROGLYGLU-----GLULYLYSHSGLYLYSVALGLYARGMETGLY 71
DB 130 GAAAAGGGGAGCCCGAGAGCTGAGAGCTGCGAGAGCTTGGCCCGGAAAAAGCAGCA 189
QY 72 PROLYSGLYILELYSGLYGLULYGLULYASPMETGLYASPARGLYASILEGLYLYSTHR 91
DB 190 CCCCAGAGATTAAAAAGAGAGGTG----- 213
QY 92 GLYPROILEGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYS 106
DB 214 GGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 273
QY 107 -----GLYILEPROGLYGLULYGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 123
DB 274 CACCCGCAAAATACAGATTGGAGCAAAATCCGGATTGGAGAGATGATTAAACGCA 333
QY 124 TYRATGLYSPHEVALGLYGLULYGLULYSPHEVALGLYGLYLYSGLYLYSGLYLYS 143
DB 334 TACAAAAAGCCTTG-----AGTTTAAAG 357
QY 144 PHEVALYASNVALLILEAGLYILEARGGLULYGLULYGLYLYSGLYLYSGLYLYSGLY 163
DB 358 GAGCTGCTAAACATT-----GGTAAAAATGTTGTCTCAACT 396
QY 164 GLINGLULYASNTYRATGLYGLULYSPHEVALGLYLYSGLYLYSGLYLYSGLYLYS 183
DB 397 GGAAGAAATATATATTGAAAGGAAATCCCTTGTGCAAAAGCTGGAAGTGTCTT 456
QY 184 ALAMETPROLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 203
DB 457 GCCTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 516
QY 204 PHEPHEVALPHEILEGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYS 223
DB 517 -----CAAGCTTATATGAGATCTGATGACAAACTGAGGCGAGATTATGACTG 570
QY 224 ASPAENTHPRILEGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 243
DB 571 AGTGTGGGCTTTA---ACTTACAGCAACTGGAACCTGGAACCAATATAT---CAC 624
QY 244 GLYHISGLYASPCYSVALGLULYGLULYGLULYGLULYGLULYGLULYGLULYGLULY 262
DB 625 AAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 684
QY 263 HISLEUTHMETTYRPHYVALCYSGLU 271
DB 685 AATTCAATATCTTCATATTTGTGAA 711

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## RESULT 2

```

US-09-198-603C-1
; Sequence 1, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: KONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC YEAST
; FILE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198,603C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Human
US-09-198-603C-1

```

## Alignment Scores:

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Score: 2.63e-24 Length: 900
Pred. No.: 289.50 Matches: 75

```

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Percent Similarity: 46.47% Conservative: 37
Best Local Similarity: 31.12% Mismatches: 100
Query Match: 19.51% Indels: 29
DB: 4 Gaps: 7

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US-09-600-932-2 (1-277) x US-09-198-603C-1 (1-900)

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QY 34 PROTHRALAGLVALCYSAALATHRHLSRTHLESER-----PROGLYPROLYSGLYASP 51
DB 162 CCGTCAAGTGTATGCTGCTGATCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 221
QY 52 ASPGLYGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 71
DB 222 GATGGCACCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 260
QY 72 PROLYSGLYILELYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 91
DB 261 CTCAGAGGCTTACAGAGGCCCCCTGGAAAGTTGGGCTCCAGAGAAATCCAGAGGCTTCT 320
QY 92 GLYPROILEGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 111
DB 321 GGGTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
QY 112 LYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 131
DB 360 AAAAGTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 410
QY 132 ASPLESERILEALARGLEULYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYS 151
DB 411 CAAACAGAAATGACACATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 458
QY 152 ILEARGLULYGLULYGLULYGLULYGLULYGLULYGLULYGLULYGLULYGLULYGLULY 171
DB 459 ---AAACAGTTGGGAAACAGTTCTTCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 515
QY 172 SERLEUTHRHISGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYS 191
DB 516 GTGAGAGCCTTGTGTGCAAGTCCAGAGCCTCTGTGCGACACCCCGAGATGCTGAGAG 575
QY 192 ASNTHREULILEALASPTRYVALALALYSERGLYPHEPHEARGVALPHEILEGLYVAL 211
DB 576 AATGAGACCTTCAATGATCATCAAGAGAG-----GAGCCTTCTGAGGCAATC 623
QY 212 ASNAPSPLEULYARGGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 231
DB 624 ACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
QY 232 SERASPTTPASNGIULYGLULYGLULYGLULYGLULYGLULYGLULYGLULYGLULYGLULY 251
DB 681 ACAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 740
QY 252 LEUSERSERGLYATGTPASAPRTHGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLYLYSGLY 271
DB 741 CTGAAAAATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
QY 272 PHE 272
DB 801 TTC 803

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## RESULT 3

```

US-09-535-521-4
; Sequence 4, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24

```



NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 876  
 TYPE: DNA  
 ORGANISM: Canis familiaris  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(876)  
 US-09-535-521-4

Alignment Scores:  
 Pred. No.: 6,79e-15 Length: 876  
 Score: 208.00 Matches: 65  
 Percent Similarity: 40.32% Conservative: 35  
 Best Local Similarity: 26.21% Mismatches: 83  
 Query Match: 14.02% Indels: 65  
 Gaps: 7

US-09-600-932-2 (1-277) x US-09-535-521-4 (1-876)

QY 68 GLYARGMETGLYPROLYSGLYILEYSGLYGLULLEUENGLYASPMETGLYASPARGLYASN 87  
 DB 183 GGTGGCGCCGCCCGCCAGACGCTCTCGGTTCCAGAG----- 221  
 QY 88 ILEGILYESTHR-----GLYPROILEGLYLYSGLYASPLYSGLYGLU 102  
 DB 222 CTGGCAAGACACACAGCGTGCAGACAGTGGCCCA----- 254  
 QY 103 LYSGLYLEULEUGLYLEPROGLYGLULYSGLYLYSALAGLYTHR-VALCYASPCYSGL 122  
 DB 255 ----GAAATCCAGAGCTGCCAGAGTGTACAGACATGAAGAAATCCAGACTGAAACAGAA 311  
 QY 122 YARGTYRARGLYSPHEVALIGLYLLEUENGLYSPLEESERILEALARGLEULYSTRSERME 142  
 DB 312 GAAATGAAGAGCTGACGAGCTGTGAGCTGCCAGAACCTGAGTGCAGCTGTTGCGAGCT 371  
 QY 142 TLSPHEVALYSPHEVALILEALAGLYLEARGGLUTHR----- 155  
 DB 372 GAACAACCTCAAGTCCAGAGCTTGAACGAGAAAGACAGCTTGACCTGACGTGAGAG 431  
 QY 155 ----- 155  
 DB 432 ACTCCAGAGAGAGGTGAGAGAGCTGTGATGAGTACACGTTCCAAAGCGCTCCGAGTG 491  
 QY 156 -----GLULYSPHEUTYRILEVALINGL 165  
 DB 492 TAACAGTCCCTGAGAGAGTGGCTCACTCCAGAGAGTGTCTACTTCTGCGGAGAG 551  
 QY 165 UGLYASANTYRARGLYSERLEUTHRHISCYARGILEARGLYGLMETLEUALAME 185  
 DB 552 GCCCAAGAGAGTGCAGAGCGCCGCTTGGCTGCACAGACGTGCAGAGCGCGCTGGCCAG 611  
 QY 185 LPROLYSASPGLUALAIALAANTHRLLEUALAASPITYRVALAIALYSSEGLYPHEPH 205  
 DB 612 CATCCACAGCCAGAGAGAGAGACTCTGCGCCAGAGTATGCCAACAAGAGGCG----- 666  
 QY 205 EARGVALPHEILEGLYVALASNPENGLUARGGLUGLYINTYRMEPHEPHTHASPAS 225  
 DB 667 ----ACCTGATTGGCTCCGCGAGCTGCAGACAGAGGGGGAGTTATCTTGATGGAGCA 722  
 QY 225 NTHPROLEUGLNASNTYRSEANTTPASNGLUGLYUPROSERASPPTYRGLYHI 245  
 DB 723 GAACCCCGT---AATATATGCAACGTGGGCGCCGAGGAGCCCAACAAGGGGCGAGCG 779  
 QY 245 SGLUASPCYSVALIGLMETLEUSERSERGLYARGTPHASPHTHGLCYSHISLEUTH 265  
 DB 780 CGAGAGAGTGCATGATGAGGCGTGGGCGAGTGAATGACGCCCTTCTGCGGAGAGTGC 839  
 QY 265 RME-----TYRPHLEVALCYSGLU 271  
 DB 840 GCTGAGAGCGCTGGGTGTGTAC 861

RESULT 4  
 US-09-535-521-6/c  
 Sequence 6, Application US/09535521  
 Patent No. 6410714  
 GENERAL INFORMATION:  
 APPLICANT: Weber, Eric R.  
 APPLICANT: McCall, Catherine A.  
 TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
 TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
 FILE REFERENCE: AL-5  
 CURRENT APPLICATION NUMBER: US/09/535,521  
 EARLIER FILING DATE: 2000-03-24  
 EARLIER APPLICATION NUMBER: 60/125,913  
 EARLIER FILING DATE: 1999-03-24  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 6  
 LENGTH: 876  
 TYPE: DNA  
 ORGANISM: Canis familiaris  
 US-09-535-521-6

Alignment Scores:  
 Pred. No.: 6,79e-15 Length: 876  
 Score: 208.00 Matches: 65  
 Percent Similarity: 40.32% Conservative: 35  
 Best Local Similarity: 26.21% Mismatches: 83  
 Query Match: 14.02% Indels: 65  
 Gaps: 7

US-09-600-932-2 (1-277) x US-09-535-521-6 (1-876)

QY 68 GLYARGMETGLYPROLYSGLYILEYSGLYGLULLEUENGLYASPMETGLYASPARGLYASN 87  
 DB 694 GGTGGCGCCGCCCGCCAGACGCTCTCGGTTCCAGAG----- 656  
 QY 88 ILEGILYESTHR-----GLYPROILEGLYLYSGLYASPLYSGLYGLU 102  
 DB 655 CTGGCAAGACACACAGCGTGCAGACAGTGGCCCA----- 623  
 QY 103 LYSGLYLEULEUGLYLEPROGLYGLULYSGLYLYSALAGLYTHR-VALCYASPCYSGL 122  
 DB 622 ----GAAATCCAGAGCTGCCAGAGTGTGATGAGTACACGATGAAGAAATCCAGACTGAAACAGAA 566  
 QY 122 YARGTYRARGLYSPHEVALIGLYLLEUENGLYSPLEESERILEALARGLEULYSTRSERME 142  
 DB 565 GAGATGAAGAGCTGACGAGCTGTGAGCTGCCAGAACCTGAGTGCAGCTGTTGCGAGCT 506  
 QY 142 TLSPHEVALYSPHEVALILEALAGLYLEARGGLUTHR----- 155  
 DB 505 GAACAACCTCAAGTCCAGAGCTTGAACGAGAAAGACAGCCTTGACCTGACGTGAGAG 446  
 QY 155 ----- 155  
 DB 445 ACTCCAGAGAGAGGTGAGAGAGCTGTGATGAGTACACGTTCCAAAGCGCTCCGAGTG 386  
 QY 156 -----GLULYSPHEUTYRILEVALINGL 165  
 DB 385 TAACAGTCCCTGAGAGAGTGGCTCACTCCAGAGAGTGTCTACTTCTGCGGAGAG 326  
 QY 165 UGLYASANTYRARGLYSERLEUTHRHISCYARGILEARGLYGLMETLEUALAME 185  
 DB 325 GCCCAAGAGAGTGCAGAGCGCCGCTTGGCTGCACAGACGTGCAGAGCGCGCTGGCCAG 266  
 QY 185 LPROLYSASPGLUALAIALAANTHRLLEUALAASPITYRVALAIALYSSEGLYPHEPH 205  
 DB 265 CATCCACAGCCAGAGAGAGAGACTCTGCGCCAGAGTATGCCAACAAGAGGCG----- 211  
 QY 205 EARGVALPHEILEGLYVALASNPENGLUARGGLUGLYINTYRMEPHEPHTHASPAS 225  
 DB 210 ----ACCTGATTGGCTCCGCGAGCTGCAGACAGAGGGGGAGTTATCTTGATGGAGCA 155  
 QY 225 NTHPROLEUGLNASNTYRSEANTTPASNGLUGLYUPROSERASPPTYRGLYHI 245





CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/453,702B  
FILING DATE: 03-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/710,955  
FILING DATE: 04-Dec-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.95017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61663  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 62:  
US-09-453-702B-62  
Alignment Scores:  
Pred. No.: 5.5e-12 Length: 61663  
Score: 206.50 Matches: 63  
Percent Similarity: 48.19% Conservative: 30  
Best Local Similarity: 32.64% Mismatches: 55  
Query Match: 13.92% Indels: 46  
DB: 4 Gaps: 8  
US-09-600-932-2 (1-277) x US-09-453-702B-62 (1-61663)  
QY 24 GlnserLeuGlyLeuAspPheSerArgProThrAlaGluValCysAlaThrHisThr 43  
DB 38638 CAGAGGCTGCACCTGCTCAGTCTGAGAGGCCA-----GACGTATG-GCTGAGAAATGCA 38690  
QY 44 IleserPro---GlyProIysGlyAspAspGlyGluIysGlyAspProGlyGluGluGly 62  
DB 38691 CGGGGGCCCCGGGGCCCTCAGAGGAAACTGTCGGAAGGGGATGTCGGTCCCTAAAGGC 38750  
QY 63 LysHisGlyLysValGlyArgMetGlyProIysGlyIleLysGlyGluLeuGlyAspMet 82  
DB 38751 GAAAGAGGTCCAGTGGCCCTCAAGGGCCCGCAAGGGCGGAAGGTGAGCGGTGAGAGCT 38810  
QY 83 GlyAspArgGlyAsnIleGlyLysThrGlyProIleGlyLysGlyAspArgGlyGlu 102  
DB 38811 GGTGCTCAGAGGGGCTGTAGGGCTGTGCTGCGGTGTGAGAAAGGGCGAAGGGGAG 38870  
QY 103 LysGlyLeuLeuGlyIlePro-----GlyGluIysGlyLysAlaGly 116  
DB 38871 CGAGAGCCGCAAGAAATACAGGCTGAAAGGGGATACCGGAGAGCGGGGCTAAAGGG 38930  
QY 117 ThrValCysAspCys-Gly---ArgTyrArgLysPheValGlyLysLeu----- 131  
DB 38931 GACCAAGGGGATATGGGCCAAGGCGAAGAGGTATCGGGAGGTCTGACGCCCG 38990  
QY 132 -----AspIle 133  
DB 38991 CAAGGTCTTAAGCGGAACGAGAGAACCCGACACAGGACCGATGGAGCAGCAGGT 39050

QY 133 eSerIleAlaArgLeuLysThrSerMetLysPheValLysAsnValIleAlaGlyIleArg 153  
DB 39051 GAGCGGGGAGAGACTGGCCCCCGAGAGTG-----AACTGGTCTGCGACGTCCG 39098  
QY 153 gGluThrGluGluLysPheTyrTyrIleValGlnGluGluLysAsnTyrArgGluSerLe 173  
DB 39099 AGAGCGGAGCAGAG-----GAGAGACCGGACCTCAGAGGAC---CT 39134  
QY 173 urHisCysArgIleArgGlyGlyMetLeuAlaMet 185  
DB 39135 CGTGAGAGCCAGGTCCGGCAGGACGCTGCAAAATG 39171  
RESULT 9  
US-09-535-521-7  
Sequence 7, Application US/09535521  
Patent No. 6410714  
GENERAL INFORMATION:  
APPLICANT: Weber, Eric R.  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)  
FILE REFERENCE: AL-5  
CURRENT APPLICATION NUMBER: US/09/535,521  
CURRENT FILING DATE: 2000-03-24  
EARLIER APPLICATION NUMBER: 60/125,913  
EARLIER FILING DATE: 1999-03-24  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 384  
TYPE: DNA  
ORGANISM: Canis familiaris  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(384)  
US-09-535-521-7  
Alignment Scores:  
Pred. No.: 8.67e-15 Length: 384  
Score: 202.50 Matches: 44  
Percent Similarity: 55.56% Conservative: 21  
Best Local Similarity: 37.61% Mismatches: 47  
Query Match: 13.65% Indels: 5  
DB: 4 Gaps: 3  
US-09-600-932-2 (1-277) x US-09-535-521-7 (1-384)  
QY 156 GluGluLysPheTyrTyrIleValGlnGluGluLysAsnTyrArgGluSerLeuThrHis 175  
DB 31 CAGAGGAAAGTGTACTGCTGCGGCGAGGACCCCAAGAACTGATCCAGGCCGGTTGCC 90  
QY 176 CysArgIleArgGlyLysMetLeuAlaMetProLysAspGluAlaAlaAsnThrLeuIle 195  
DB 91 TGCAGAGAGCTGCAGAGGGGCGCTGGCCAGCATCCACAGCCAAAGAGAGCAGGACTTCTCG 150  
QY 196 AlaAspTyrValAlaLysSerGlyPhePheArgValPheIleGlyValAsnAspLeuGlu 215  
DB 151 GCCAGGTATGCCAACAAGAGGCG-----ACCTGATTTGGCTCCGGGACCTGGAGC 201  
QY 216 ArgGluGlyGlnTyrMetPheThrAspAsnThrProLeuGlnAsnTyrSerAsnThrPasn 235  
DB 202 AGAGAGGGGAGATTATCTGATGAGAGCAACCCCTG---AACTATGCAACTGGCGG 258  
QY 236 GluGluGluProSerAspProTyrGlyHisGluAspCysValGluMetLeuSerSerGly 255  
DB 259 CCGGGGAGCCCAACAACGAGGGGCGGCGAGGACATGCTGATGATGACAGGGCTCGGGG 318  
QY 256 ArgTyrAsnAspThrGluCysHisLeuThrMet---TyrPheValCysGlu 271  
DB 319 CAGTGAATGACCGCTTCTGCGGACAGCTCGTGGAGCGCTGGTGTGTGAC 369  
RESULT 10

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US-09-535-521-9/C
; Sequence 9, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-9

Alignment Scores:
Pred. No.: 8,67e-15 Length: 384
Score: 202.50 Matches: 44
Percent Similarity: 55.56% Conservative: 21
Best Local Similarity: 37.61% Mismatches: 47
Query Match: 13.65% Indels: 5
DB: GAPS: 3

US-09-600-932-2 (1-277) x US-09-535-521-9 (1-384)
QY 156 GUGLUYSPhetyrTYrILEValGInGLuLUysaNTYrArgLUserLeuThrHis 175
DB 354 CAGAGGAAGTGTACTACTTCGGGAGAGAGCCCAAGAGTGCAGGCCCGTTGGCC 295
QY 176 CysArgILEarGLyGLyMeLUeLUaMeLProLYsaPGLuAlaLAsnThrLeuile 195
DB 234 TGCACCAAGCTGCAGAGGGCGTCCGACATCCACAGCCAGAGGAGCAGACTTCCTG 235
QY 196 AlaAspTYrValAlaLYsSerGLyPhePheArGLyValPheILEGLyValAsnAspLeuLU 215
DB 234 GCCAGGTATGCCAACAAAGAGGC-----ACCTGATGCGCTCCGGAGCTGGAC 184
QY 216 ArgGLyGLyInTYrMeLpHeThrAspAsnThrProLeuGLuInAsnTYrSerAsnTrpAsn 235
DB 183 AGAGAGGGGGAGTTATCTGTGATGACGAGAACCCCTG---AACTATAGCAACTGGCG 127
QY 236 GUGLUYLUProSerAspProTYrGLyHISGLuAspCYsValGLuMeLUeLUserSergLY 255
DB 126 CCGGGGAGCCCAACAGCGGGGCCAGGCGCAGAGACTGCGTGTATGATGCAGAGGCTGGGG 67
QY 236 ArgTrpAsnAspThrGLyCysHISLeuThrMet---TYrPheValCYsGLu 271
DB 66 CAGTGGATATGACGCTTCTGCGGCGACGCTGAGACGGCTGGGTGTGTGAC 16

RESULT 11
US-09-535-521-10
; Sequence 10, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 417
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TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(417)
US-09-535-521-10

Alignment Scores:
Pred. No.: 9.79e-15 Length: 417
Score: 202.50 Matches: 44
Percent Similarity: 55.56% Conservative: 21
Best Local Similarity: 37.61% Mismatches: 47
Query Match: 13.65% Indels: 5
DB: GAPS: 3

US-09-600-932-2 (1-277) x US-09-535-521-10 (1-417)
QY 156 GUGLUYSPhetyrTYrILEValGInGLuLUysaNTYrArgLUserLeuThrHis 175
DB 64 CAGAGGAAGTGTACTACTTCGGGAGAGAGCCCAAGAGTGCAGGCCCGTTGGCC 123
QY 176 CysArgILEarGLyGLyMeLUeLUaMeLProLYsaPGLuAlaLAsnThrLeuile 195
DB 124 TGCACCAAGCTGCAGAGGGCGTCCGACATCCACAGCCAGAGGAGCAGACTTCCTG 183
QY 196 AlaAspTYrValAlaLYsSerGLyPhePheArGLyValPheILEGLyValAsnAspLeuLU 215
DB 184 GCCAGGTATGCCAACAAAGAGGC-----ACCTGATGCGCTCCGGAGCTGGAC 234
QY 216 ArgGLyGLyInTYrMeLpHeThrAspAsnThrProLeuGLuInAsnTYrSerAsnTrpAsn 235
DB 235 AGAGAGGGGAGTTATCTGTGATGACGAGAACCCCTG---AACTATAGCAACTGGCG 291
QY 236 GUGLUYLUProSerAspProTYrGLyHISGLuAspCYsValGLuMeLUeLUserSergLY 255
DB 292 CCGGGGAGCCCAACAGCGGGGCCAGGCGCAGAGACTGCGTGTATGATGCAGAGGCTGGGG 351
QY 256 ArgTrpAsnAspThrGLyCysHISLeuThrMet---TYrPheValCYsGLu 271
DB 352 CAGTGGATATGACGCTTCTGCGGCGACGCTGAGACGGCTGGGTGTGTGAC 402

RESULT 12
US-09-535-521-12/C
; Sequence 12, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-12

Alignment Scores:
Pred. No.: 9.79e-15 Length: 417
Score: 202.50 Matches: 44
Percent Similarity: 55.56% Conservative: 21
Best Local Similarity: 37.61% Mismatches: 47
Query Match: 13.65% Indels: 5
DB: GAPS: 3

US-09-600-932-2 (1-277) x US-09-535-521-12 (1-417)
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